

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:44:55 ; Search time 4576.22 Seconds
(without alignments)
21.890 Million cell updates/sec

Title: US-08-943-144-13
Perfect score: 28
Sequence: 1 GATTGCTCAACACAGAGTAGTGCCTAC 28

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

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39: gb_pl2: *
40: gb_pl1: *
41: gb_pl2: *
42: gb_pr3: *
43: gb_sts: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

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7	19	67.9	4293	8	TOBPHYB	L10114 Nicotiana tub
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11	19	67.9	4904	38	S51538	Y14676 Nicotiana p
12	19	67.9	4907	38	STPHYB	Y14676 Nicotiana p
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ALIGNMENTS

RESULT 1
D88452
LOCUS D88452 433 bp mRNA 10-NOV-1997
DEFINITION Zea mays mRNA for aldehyde oxidase-2, complete cds.
ACCESSION D88452
NID 92589163
KEYWORDS aldehyde oxidase-2; zmao-2.
SOURCE Zea mays coleoptile CDNA to mRNA.
ORGANISM Zea mays

REFERENCE
Eukaryotae: Viridiplantae: Charophyta/Embryophyta group;
Embryophyta: vascular plants; seed plants; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (sites)

SEKIMOTO, H., Seo, M., Dojima, N., Takio, K., Kamiya, Y. and Koshiba, T.
Cloning and molecular characterization of plant aldehyde oxidase
J. Biol. Chem. 272 (24), 15280-15285 (1997)
97326103
REFERENCE
2 (bases 1 to 4333)
SEKIMOTO, H.
Direct Submission
Submitted (19-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hiroaki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirosawa 2-1, Wako, Saitama 351-01,

FEATURES

source

Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)

Location/Qualifiers

1..4333

/organism="Zea mays"

/db_xref="taxon:4577"

/tissue_type="coleoptile"

/gene="zmao-2"

/gene="zmao-2"

/note="putative"

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polyA_site

/note="26 A nucleotides"

BASE COUNT

1120 a 1056 c 1138 g 1019 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 8; Length 4333;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTGCTCAACACAGAGTATGCTTAC 28

Db 2121 GATTGCTCAACACAGAGTATGCTTAC 2148

RESULT 2

LOCUS

D88452 4333 bp mRNA PLN 10-NOV-1997

DEFINITION

Zea mays mRNA for aldehyde oxidase-2, complete cds.

ACCESSION

D88452

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

TITLE

JOURNAL

Direct Submission
Submitted (19-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirosewa 2-1, Wako, Saitama 351-01,
Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)

Location/Qualifiers

1..4333

/organism="Zea mays"

/db_xref="taxon:4577"

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polyA_site

/note="26 A nucleotides"

BASE COUNT

1120 a 1056 c 1138 g 1019 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 38; Length 4333;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTGCTCAACACAGAGTATGCTTAC 28

Db 2121 GATTGCTCAACACAGAGTATGCTTAC 2148

RESULT 3

LOCUS

ONU58368 7049 bp DNA INV 16-OCT-1996

DEFINITION

Oxytricha nova

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

A gene-sized DNA molecule encoding the catalytic subunit of DNA

Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)

FEATURES

source

1. .4333
/organism="Zea mays"
/db_xref="taxon:4577"
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CDS

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BASE COUNT 1120 a 1056 c 1138 g 1019 t
ORIGIN

Query Match 100.0%; Score 24; DB 8; Length 4333;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCACCTATGCTGCAGTTC 24
Db 1147 TTCCACCTATGCTGCAGTTC 1124

RESULT 2
LOCUS D88452 4333 bp mRNA PLN 10-NOV-1997
DEFINITION Zea mays mRNA for aldehyde oxidase-2, complete cds.
ACCESSION D88452
NID 92589163
KEYWORDS aldehyde oxidase-2; zmao-2.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL J Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4333)
AUTHORS Sekimoto, H.

TITLE

JOURNAL

Direct Submission
Submitted (19-OCT-1996) to the DBJ/EMBL/GenBank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirosewa 2-1, Wako, Saitama 351-01,
Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)

FEATURES

source

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91. .4140
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VKEELGDLVVERYLESVASAPVTATANA"

polyA_site

BASE COUNT 1120 a 1056 c 1138 g 1019 t
ORIGIN

Query Match 100.0%; Score 24; DB 38; Length 4333;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCACCTATGCTGCAGTTC 24
Db 1147 TTCCACCTATGCTGCAGTTC 1124

RESULT 3
LOCUS D88451 4382 bp mRNA PLN 10-NOV-1997
DEFINITION Zea mays mRNA for aldehyde oxidase, complete cds.
ACCESSION D88451
NID 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL J Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4333)
AUTHORS Sekimoto, H.

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:45:23 ; Search time 4576.22 Seconds
(without alignments)
18.762 Million cell updates/sec

Title: US-08-943-144-15

Sequence: 1 TTCACCTATGCTGCAGTGTCC 24

Scoring table: IDENTITY_NUC

Searched: 808301 segs, 178873984 residues

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:44:20 ; Search time 4576.22 Seconds

(Without alignments)
21.890 Million cell updates/sec

Title: US-08-943-144-8

Perfect score: 28
Sequence: 1 GATGCTGAACACAAAGATATGCTAAT 28

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

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1: gb_ba1:*
2: gb_ba2:*
3: gb_in:*
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22: em_hum2:*
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38: gb_pl1:*
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41: gb_pr2:*
42: gb_pr3:*
43: gb_sts:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

1	28	100.0	4382	8	D88451	D88451 Zee mays mr
2	28	100.0	4382	38	D88451	D88451 Zee mays mr
3	21	75.0	2707	5	TKYRPL	L76587 Metlegris g
4	20	71.4	46899	6	A36768	A36768 Sequence 1
5	20	71.4	46899	8	TISACYS	Z28383 T.niveum (A
6	20	71.4	136755	11	AC002529	AC002529 Human BAC
7	20	71.4	126955	11	AC004773	AC004773 Homo sapi
8	20	71.4	46899	38	TISACYS	Z28383 T.niveum (A
9	20	71.4	136755	41	AC002529	AC002529 Human BAC
10	20	71.4	126955	41	AC004773	AC004773 Homo sapi
11	19.8	70.7	162691	18	AC003061	AC003061 *** SEQUE
12	19.6	70.0	719	5	AF015303	AF015303 Xenopus I
13	19.6	70.0	2957	8	SCYJL156C	Z49431 S.cerevisia
14	19.6	70.0	3941	8	SCYJL157C	Z49432 S.cerevisia
15	19.6	70.0	73031	11	HS84917	Z82217 Human DNA S
16	19.6	70.0	128169	11	HS84917	AL008987 Human DNA
17	19.6	70.0	107910	11	HUAC002394	AC002394 Human Chr
18	19.6	70.0	1069	17	HUAC002394	Z82579 R.prowazeki
19	19.6	70.0	1145	17	PAP20NIB	AF062348 Plasmodu
20	19.6	70.0	1145	17	PAP20NIB	AF062349 Plasmodu
21	19.6	70.0	2565	17	WTVPNS4A	Z81472 Caenorhabdi
22	19.6	70.0	2957	38	SCYJL156C	Z68013 Caenorhabdi
23	19.6	70.0	3941	38	SCYJL157C	M37213 P.falciparu
24	19.6	70.0	73031	41	HS7883	M19143 P.falciparu
25	19.6	70.0	128169	41	HS7883	M35727 P.falciparu
26	19.6	70.0	107910	41	HS84917	X03831 P.falciparu
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28	19.6	70.0	312430	2	RPXX02	X0087 Plasmodium
29	19.6	70.0	5243	3	AF062348	Y05624 Plasmodium
30	19.6	70.0	5221	3	AF062349	AC004160 Homo sapi
31	19.6	70.0	30451	3	CEC16D6	AF042090 Homo sapi
32	19.6	70.0	17716	3	CEC16D6	Z46386 Bovine hept
33	19.6	70.0	5276	3	PFAP195	Z82579 R.prowazeki
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35	19.6	70.0	3518	3	PFAP190A	Z68013 Caenorhabdi
36	19.6	70.0	5541	3	PRGP195	M37213 P.falciparu
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39	19.6	70.0	143751	11	AC004160	X03831 P.falciparu
40	19.6	70.0	155407	11	AF042090	Z35327 P.falciparu
41	19.6	70.0	4179	17	BHVAREGE	Y0087 Plasmodium
42	19.6	70.0	241	36	RPX02	X05624 Plasmodium
43	19.6	70.0	312430	37	RPX02	AC004160 Homo sapi
44	19.6	70.0	143751	41	AC004160	AF042090 Homo sapi
45	19.6	70.0	155407	41	AF042090	Z46386 Bovine hept

ALIGNMENTS

RESULT 1
D88451 4382 bp mRNA PLN 10-NOV-1997
LOCUS Zee mays mRNA for aldehyde oxidase, complete cds.
DEFINITION D88451
ACCESSION 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zee mays coleoptile cDNA to mRNA.
ORGANISM Zee mays

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshida, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL J. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4382)
AUTHORS Sekimoto, H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1996) to the DDBJ/EMBL/Genbank databases.
Hirotsuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirotsuki 2-1, Wako, Saitama 351-01,

Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)
Location/Qualifiers

FEATURES

source

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/tissue_type="coleoptile"
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4382

CDS

polyA_site

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ORIGIN /note="30 A nucleotides"

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Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTGCTGAACACAAAGATATGCTAAT 28
Db 2100 GATTGCTGAACACAAAGATATGCTAAT 2127

RESULT 2
LOCUS D88451 4382 bp mRNA PLN 10-NOV-1997
DEFINITION Zea mays mRNA for aldehyde oxidase, complete cds.
ACCESSION D88451
NID 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays

REFERENCE
1 (sites)
Sakimoto, H., Seo, M., Doi, M., Takio, K., Kamuya, Y. and Koshiba, T.
Cloning and molecular characterization of plant aldehyde oxidase
J. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4382)
Sakimoto, H.

TITLE

JOURNAL

Direct Submission
Submitted (19-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hiroshima 2-1, Wako, Saitama 351-01,
Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)

FEATURES

source

1.4382
/organism="Zea mays"
/db_xref="taxon:4577"
/tissue_type="coleoptile"
46..4122
/gene="zmao-1"
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MDVPATMPVVKELGIDVVERYLENVSAAAGPNTAKA"
4382

CDS

polyA_site

BASE COUNT 1163 a 1061 c 1142 g 1016 t
ORIGIN /note="30 A nucleotides"

Query Match 100.0%; Score 28; DB 38; Length 4382;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTGCTGAACACAAAGATATGCTAAT 28
Db 2100 GATTGCTGAACACAAAGATATGCTAAT 2127

RESULT 3
LOCUS TKYTPRL 2707 bp mRNA VRT 30-MAY-1996
DEFINITION Melagris gallopavo prolactin receptor (tpplr) mRNA, complete cds.
ACCESSION U76587
NID 91345364
KEYWORDS prolactin receptor.
SOURCE Melagris gallopavo female immature kidney cDNA to mRNA.
ORGANISM Melagris gallopavo

REFERENCE
1 (bases 1 to 2707)
Zhou, J.F., Zadororny, D., Guemene, D. and Kunhlein, U.
Molecular cloning, tissue distribution and expression during

Direct Submission
Submitted (19-Oct-1996) to the DDBJ/EMBL/Genbank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research
Frontier Research Program; Hirotsuwa 2-1, Wako, Saitama 351-01,

Description:

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:44:50 ; Search time 4576.22 Seconds
(without alignments)
18.762 Million cell updates/sec

Title: US-08-943-144-12
Perfect score: 24
Sequence: 1 ATCGACCTGTGTCGGCCTGAC 24

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 178873984 residues

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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41: gb_vl: *
42: gb_vl: *
43: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

C	1	24	100.0	4382	8	D88451	D88451 Zea mays mr
C	2	24	100.0	4382	38	D88451	D88451 Zea mays mr
C	3	18.2	75.8	44000	18	AC005929	AC005929 *** SEQUE
C	4	17.8	74.2	2818	1	AGDNAKGE	X87113 A. tumefaci
C	5	17.8	74.2	4617	1	PAU27829	U27829 Pseudomonas
C	6	17.8	74.2	1786	1	PSEALGLA	L14597 Pseudomonas
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C	10	17.6	73.3	19493	1	D90826	D90826 E. coli geno
C	11	17.6	73.3	18886	1	D90827	D90827 E. coli geno
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C	13	17.6	73.3	6327	6	A56817	A56817 Sequence 1
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C	40	16.6	69.2	189370	1	AF010496	AF010496 Rhodobact
C	41	16.6	69.2	3817	1	AF019251	AF019251 Brucella
C	42	16.6	69.2	4972	1	MAMAMIRM	X79027 M. ammoniaph
C	43	16.6	69.2	8008	1	PAU93274	U93274 Pseudomonas
C	44	16.6	69.2	2655	1	PGICFXHYEP	M64172 Plasmid phg
C	45	16.6	69.2	1280	1	RCU14593	U14593 Rhodobacter

ALIGNMENTS

RESULT 1
D88451/c 4382 bp mRNA PLN 10-NOV-1997
LOCUS Zea mays mRNA for aldehyde oxidase, complete cds.
DEFINITION D88451
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryotes; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.

REFERENCE

1 (sites)
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL J. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 9736103
REFERENCE 2 (bases 1 to 4382)
AUTHORS Sekimoto, H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hirotsuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirotsuki 2-1, Wako, Saitama 351-01,

Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)
Location/Qualifiers

FEATURES

source
1. 4382
/organism="Zea mays"
/db_xref="taxon:4577"
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polyA_site

BASE COUNT 1163 a 1061 c 1142 g 1016 t
ORIGIN

Query Match 100.0%; Score 24; DB 8; Length 4382;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCGACTTGTGCGGCTTGAC 24
Db 474 ATCGACTTGTGCGGCTTGAC 451

RESULT 2
LOCUS D88451 4382 bp mRNA PLN 10-NOV-1997
DEFINITION Zea mays mRNA for aldehyde oxidase, complete cds.
ACCESSION D88451
NID 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (sites)

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Doi, M., N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
J. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4382)
AUTHORS Sekimoto, H.

TITLE

Direct Submission
Submitted (19-OCY-1996) to the DBJ/EMBL/GenBank databases.
Hiroaki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirosewa 2-1, Wako, Saitama 351-01,
Japan (E-mail: sekimoto@postman.riken.go.jp, Tel: +81-48-462-1111,
Fax: +81-48-462-4691)
Location/Qualifiers

FEATURES

source
1. 4382
/organism="Zea mays"
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46. 4122
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polyA_site

BASE COUNT 1163 a 1061 c 1142 g 1016 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCGACTTGTGCGGCTTGAC 24
Db 474 ATCGACTTGTGCGGCTTGAC 451

RESULT 3
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DEFINITION *** SEQUENCING IN PROGRESS *** Leishmania major chromosome 3 clone
ACCESSION AC005929
NID 93850589
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 44000)
REFERENCE Myler, P.J., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M.,
Cawthra, J., Marsolun, F., Sunkin, S. and Stuart, K.D.

Japan (E-mail:sekimoto@postman.riken.go.jp, Tel:+81-48-462-1111,
Fax:+81-48-462-4691)

FEATURES

source

Location/Qualifiers
1. .4382

/organism="Zea mays"
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CDS

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGCCTTTGGAGCCACTGGA 24
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LOCUS D88452
DEFINITION D88452
ACCESSION D88452
NID 92589163
KEYWORDS aldehyde oxidase-2; zmao-2.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Liliopsida; Poales; Poaceae; Zea.

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL J. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97362103
REFERENCE 2 (bases 1 to 4333)
AUTHORS Sekimoto, H.

TITLE

JOURNAL

Direct Submission
Submitted (19-OCT-1996) to the DDBJ/EMBL/Genbank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirotsu 2-1, Wako, Saitama 351-01,
Japan (E-mail:sekimoto@postman.riken.go.jp, Tel:+81-48-462-1111,
Fax:+81-48-462-4691)

FEATURES

source

Location/Qualifiers
1. .4333

/organism="Zea mays"
/db_xref="taxon:4577"
/tissue-type="coleoptile"

gene

CDS

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polya_site

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGCCTTTGGAGCCACTGGA 24
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RESULT 3
D88451/c 4382 bp mRNA PLN 10-NOV-1997
LOCUS D88451
DEFINITION D88451
ACCESSION D88451
NID 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Liliopsida; Poales; Poaceae; Zea.

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohmae, N., Takio, K., Kamiya, Y. and Koshiba, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:44:40 ; Search time 4576.22 seconds
(without alignments)
18.762 Million cell updates/sec

Title: US-08-943-144-11
Perfect score: 24
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Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	22	17.2	71.7	40301	3	CELD1044	U00065 Caenorhabdi
C	23	17.2	71.7	3613	10	HUMAPO44A	J02758 Human apoli
C	24	17.2	71.7	4306	10	HUMCAD	M38561 Human apoli
C	25	17.2	71.7	2858	10	MEAPO44A	X68361 M.fascicula
C	26	17.2	71.7	51476	11	HS503F6	AL021153 Homo sapi
C	27	17.2	71.7	33608	13	AC003057	AC003057 Mouse Cos
C	28	17.2	71.7	1660	13	RATSTLD	D16300 Rat RNA fo
C	29	17.2	71.7	180942	18	AC005874	AC005874 *** SEQUE
C	30	17.2	71.7	112313	18	HS1172A22	AL034386 Human DNA
C	31	17.2	71.7	140907	18	HS163G9	AL008733 Human DNA
C	32	17.2	71.7	4306	40	HUMAPO44A	J02758 Human apoli
C	33	17.2	71.7	4306	40	HUMCAD	M38561 Human apoli
C	34	17.2	71.7	2858	40	MEAPO44A	X68361 M.fascicula
C	35	17.2	71.7	51476	41	HS503F6	AL021153 Homo sapi
C	36	17.2	71.7	514	43	HUMUT541	L16277 Human chrom
C	37	16.8	70.0	1714	3	DNMSD	X55676 D. melanoga
C	38	16.8	70.0	3946	3	DMU51044	U51044 Drosophila
C	39	16.8	70.0	94752	11	AC003098	AC003098 Homo sapi
C	40	16.8	70.0	250599	11	AF015262	AF015262 Homo sapi
C	41	16.8	70.0	40697	11	AF039905	AF039905 Homo sapi
C	42	16.8	70.0	100000	11	AP000043	AP000043 Homo sapi
C	43	16.8	70.0	288002	11	HS229043	AJ229043 Homo sapi
C	44	16.8	70.0	1356	13	MMU55040	U55040 Mus musculu
C	45	16.8	70.0	94752	41	AC003098	AC003098 Homo sapi

ALIGNMENTS

RESULT 1
D88451/c
LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

D88451 4382 bp mRNA PLN 10-NOV-1997
D88451 Zea mays mRNA for aldehyde oxidase, complete cds.
g2589161
aldehyde oxidase; zmao-1.
Zea mays coleoptile cDNA to mRNA.
Zea mays
Eukaryotae: Viridiplantae: Charophyta/Embryophyta group:
Embryophyta: vascular plants: seed plants: Magnoliophyta:
Liliopsida: Poales: Poaceae: Zea.
1 (sites)
Sekimoto,H., Seo,M., Dojmae,N., Takio,K., Kamiya,Y. and Koshiba,T.
Cloning and molecular characterization of plant aldehyde oxidase
J. Biol. Chem. 272 (24), 15280-15285 (1997)
97326103
2 (bases 1 to 4382)
Sekimoto,H.
Direct Submission
Submitted (19-OCT-1996) to the DDBJ/EMBL/Genbank databases.
Hiroyuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirosewa 2-1, Wako, Saitama 351-01,

RESULT 2
US-08-552-142A-1/C
; Sequence 1, Application US/08552142A
; Patent No. 5695995
; GENERAL INFORMATION:
; APPLICANT: Weintraub, Harold M.
; APPLICANT: Lee, Jacqueline E.
; APPLICANT: Tapscott, Stephen J.
; APPLICANT: Hollenberg, Stanley M.
; TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/552,142A
; FILING DATE: 02-NOV-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,238
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05741
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: FPCR-1-8933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-225-0709
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2089 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 229..1302
; US-08-552-142A-1

Query Match 60.0%; Score 16.2; DB 2; Length 2089;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CTTTGACGACATATTAGCATA 23
|||||
Db 1403 CTTTGACGACATATTAGCATA 1383

RESULT 3
US-08-910-973-1/C
; Sequence 1, Application US/08910973
; Patent No. 5795723
; GENERAL INFORMATION:
; APPLICANT: Tapscott, Stephen J.
; APPLICANT: Olson, James M.

; TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectod
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,973
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,238
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05741
; FILING DATE: 08-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17532
; FILING DATE: 30-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FPCR-1-10958
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100; 206-224-0735 (direct)
; TELEFAX: 206-225-0779
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2089 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 229..1302
; US-08-910-973-1

Query Match 60.0%; Score 16.2; DB 3; Length 2089;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CTTTGACGACATATTAGCATA 23
|||||
Db 1403 CTTTGACGACATATTAGCATA 1383

RESULT 4
PCT-US93-03077-2/C
; Sequence 2, Application PC/TUS9303077
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Wu, Foon Kiu
; TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
; TITLE OF INVENTION: REGULATING GENE EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas

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OM nucleic - nucleic search, using sw model

Run on: July 15, 1999, 00:27:44 ; Search time 269.22 seconds
(without alignments)
18.868 Million cell updates/sec

Title: US-08-943-144-9
Perfect score: 27
Sequence: 1 TGGCTGCAGATTTCGTCTACTACTC 27

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	27	1	V40722	Primer for aldehyd
2	27	100.0	4412	1	V40710	Aldehyde oxidase g
3	27	100.0	4359	1	V40711	Aldehyde oxidase g
4	27	100.0	27	1	V40716	Primer for aldehyd
5	18	66.7	3902	1	V52345	Streptococcus pneu
6	18	66.7	3189	1	V65242	DNA encoding three
7	17.6	65.2	1524	1	T40119	Human papillomavir
8	17.6	65.2	455	1	T91248	Human papilloma vi
9	17.2	63.7	621	1	N93068	Sequence of phosph
10	17	63.0	3158	1	Q31880	Cyclin D3 promoter
11	17	63.0	3158	1	O53212	Human cyclin D3 pr
12	17	63.0	2088	1	O67458	Codes (opt) synthe
13	17	63.0	387	1	T85540	gpi2 (opt) synthe
14	17	63.0	387	1	V21766	HIV gpi2 (opt) gen
15	16.6	61.5	422	1	T80646	Type II topoisomer
16	16.4	60.7	3091	1	N90387	Gene encoding KEX2
17	16.4	60.7	3275	1	N97129	Partial sequence o
18	16.4	60.7	3442	1	O20545	Encodes KEX2 endop
19	16.4	60.7	5108	1	O53403	Sequence encoding
20	16.4	60.7	4106	1	O98696	Yeast KEX2 gene. Y
21	16.4	60.7	5077	1	O97812	Sequence encoding
22	16.4	60.7	19307	1	T27558	Shuttle vector pad
23	16.4	60.7	2434	1	T27048	STR4 (suppressor o
24	16.4	60.7	2703	1	T28403	E. coli detection
25	16.4	60.7	1166	1	T72146	Pea type I lncitb
26	16.4	60.7	4590	1	T94612	Rat penile neurona
27	16.4	60.7	2328	1	T95227	Human islet cell a
28	16.4	60.7	2848	1	T86089	Kex2 protease enco
29	16.4	60.7	455	1	V09022	Homo sapiens 20q13
30	16.4	60.7	13815	1	V18885	Mus musculus dyster
31	16.4	60.7	2437	1	T84149	DNA encoding one u
32	16.4	60.7	3495	1	V47506	glutrinagin amidotr
33	16.4	60.7	2437	1	V53491	DNA encoding a sta
34	16.4	60.7	5910	1	V66798	Rice bacterial lea
35	16.2	60.0	3452	1	V57908	Bovine butyrophill
36	16.2	60.0	3083	1	V69301	Human OGT DNA. Pro
37	16	59.3	2610	1	O32656	LEM1 8 cDNA. New
38	16	59.3	3059	1	V42652	Nucleotide sequenc
39	16	59.3	5099	1	V38239	Nucleotide sequenc
40	16	59.3	10708	1	V69286	Sequence of mouse
41	15.8	58.5	2839	1	O03742	Human SKI related
42	15.8	58.5	1629	1	O62313	Rat somatoliberin
43	15.8	58.5	2914	1	O70813	Protein kinase (CK

44 15.8 58.5 3975 1 O92412
45 15.8 58.5 2914 1 O92948

ALIGNMENTS

RESULT 1
ID V40722 standard; DNA; 27 BP.
AC V40722;
DT 22-SEP-1998 (first entry)
DE Primer for aldehyde oxidase gene.
KW Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.
OS Synthetic.
OS Zea mays.
PN EP-834558-A2.
PD 08-APR-1998.
PF 02-OCT-1997; 117168.
PR 04-OCT-1996; JP-283314.
PA (SUMO) SUMITOMO CHEM CO LTD.
PI Koshida T.
DR WPI: 98-195460/18.
PT Aldehyde oxidase gene from plants and related vector and transformed cells - particularly for modulating auxin production in plants to accelerate maturation, increase yield, induce dwarfing etc.
PS Example 8; Page 7; 34pp; English.
CC This sequence represents a primer for the DNA encoding the Zea mays aldehyde oxidase protein of the invention. The enzyme is able to oxidise an aldehyde to carboxylic acid (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells transformed with the DNA are used to express the enzyme. Specifically expression of the DNA in transformed CC plants is used to increase (or suppress) production and activity of auxin, e.g. to cause earlier maturation of crops, improved yields and CC quality of fruit, to prevent weak growth, to develop strains able to grow under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging CC in rice) and to shorten flowers. Also plant cells that over-express the CC DNA can be proliferated, differentiated and regenerated in sterile CC medium, particularly for production of virus-free nursery stock (of CC flowers or ornamental plants).
SQ Sequence 27 BP: 4 A; 6 C; 6 G; 11 T;

Query Match 100.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGCTGCAGATTTCGTCTACTACTC 27
Db 1 TGGCTGCAGATTTCGTCTACTACTC 27

RESULT 2
ID V40710 standard; cDNA to mRNA; 4412 BP.
AC V40710;
DT 22-SEP-1998 (first entry)
DE Aldehyde oxidase gene.
KW Aldehyde oxidase; auxin production; plant maturation; ss.
OS Zea mays.
PN Key
FT CDS Location/Qualifiers
FT CDS 46..412 /*tag= a
FT EP-834558-A2.
PD 08-APR-1998.
PF 02-OCT-1997; 117168.
PR 04-OCT-1996; JP-283314.
PA (SUMO) SUMITOMO CHEM CO LTD.
PI Koshida T.
DR WPI: 98-195460/18.
PT P-PSDB; W57837.
PT Aldehyde oxidase gene from plants and related vector and transformed cells - particularly for modulating auxin production in plants to

PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Claim 3: Page 17-21: 34pp: English.
 CC This sequence encodes the *zea mays* aldehyde oxidase protein of the
 CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
 CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
 CC transformed with the DNA are used to express the enzyme. Specifically
 CC expression of the DNA in transformed plants is used to increase (or
 CC suppress) production and activity of auxin, e.g. to cause earlier
 CC maturation of crops, improved yields and quality of fruit, to prevent
 CC weak growth, to develop strains able to grow under suboptimal conditions,
 CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
 CC flowering. Also plant cells that over-express the DNA can be proliferated,
 CC differentiated and regenerated in sterile medium, particularly for
 CC production of virus-free nursery stock (of flowers or ornamental plants).
 SQ Sequence 4412 BP; 1193 A; 1061 C; 1142 G; 1016 T;

Query Match 100.0%; Score 27; DB 1; Length 4412;
 Best Local Similarity 100.0%; Pred. No. 0.00096;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGCTGCAGATTTCGTCTATCTC 27
 DB 2178 TGGCTGCAGATTTCGTCTATCTC 2152

RESULT 3
 ID V40711/c
 AC V40711:
 DT 22-SEP-1998 (first entry)
 DE Aldehyde oxidase gene.
 KW Aldehyde oxidase; auxin production; plant maturation; ss.
 OS *zea mays*.
 FH Key
 FT CDS Location/Qualifiers
 FT 91..414
 FT EP-834558-A2.
 PD 08-APR-1998.
 PF 02-OCT-1997; 117168.
 PR 04-OCT-1996; JP-283314.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Koshiba T;
 DR WPI: 98-195460/18.
 DR P-PSDB: W57838.
 PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Claim 3: Page 30-34; 34pp: English.
 CC This sequence encodes the *zea mays* aldehyde oxidase protein of the
 CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
 CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
 CC transformed with the DNA are used to express the enzyme. Specifically
 CC expression of the DNA in transformed plants is used to increase (or
 CC suppress) production and activity of auxin, e.g. to cause earlier
 CC maturation of crops, improved yields and quality of fruit, to prevent
 CC weak growth, to develop strains able to grow under suboptimal conditions,
 CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
 CC flowering. Also plant cells that over-express the DNA can be proliferated,
 CC differentiated and regenerated in sterile medium, particularly for
 CC production of virus-free nursery stock (of flowers or ornamental plants).
 SQ Sequence 4359 BP; 1146 A; 1056 C; 1138 G; 1019 T;

Query Match 100.0%; Score 27; DB 1; Length 4359;
 Best Local Similarity 100.0%; Pred. No. 0.00096;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGCTGCAGATTTCGTCTATCTC 27
 DB 2199 TGGCTGCAGATTTCGTCTATCTC 2173

RESULT 4
 ID V40716
 AC V40716:
 DT 22-SEP-1998 (first entry)
 DE Primer for aldehyde oxidase gene.
 KW Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.
 OS Synthetic.
 FH *zea mays*.
 FT EP-834558-A2.
 PD 08-APR-1998.
 PF 02-OCT-1997; 117168.
 PR 04-OCT-1996; JP-283314.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Koshiba T;
 DR WPI: 98-195460/18.
 PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Example 8: Page 7; 34pp: English.
 CC This sequence represents a primer for the DNA encoding the *zea mays*
 CC aldehyde oxidase protein of the invention. The enzyme is able to oxidise
 CC an aldehyde to carboxylic acid (specifically indole acetaldehyde to
 CC indole acetic acid (auxin)). Cells transformed with the DNA are used to
 CC express the enzyme. Specifically expression of the DNA in transformed
 CC plants is used to increase (or suppress) production and activity of
 CC auxin, e.g. to cause earlier maturation of crops, improved yields and
 CC quality of fruit, to prevent weak growth, to develop strains able to grow
 CC under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging
 CC in rice) and to shorten flowering. Also plant cells that over-express the
 CC DNA can be proliferated, differentiated and regenerated in sterile
 CC medium, particularly for production of virus-free nursery stock (of
 CC flowers or ornamental plants).
 SQ Sequence 27 BP; 4 A; 6 C; 6 G; 11 T;

Query Match 100.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00038;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGCTGCAGATTTCGTCTATCTC 27
 DB 1 TGGCTGCAGATTTCGTCTATCTC 27

RESULT 5
 ID V52345/c
 AC V52345:
 DT 23-OCT-1998 (first entry)
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:212.
 KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 KW computer readable medium; vaccine; pharmaceutical composition; ds.
 OS Streptococcus pneumoniae.
 PN W09818931-A2.
 PD 07-MAY-1998.
 PF 30-OCT-1997; 019588.
 PR 31-OCT-1996; US-029960.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash CA, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
 PI Kunsch CA, Rosen CA;
 DR WPI: 98-272225/24.
 PT Computer-readable medium with recorded Streptococcus pneumoniae
 PT polynucleotide sequences - useful in diagnostic kits and assays, and
 PT pharmaceutical compositions and vaccines for Streptococcus
 PT pneumoniae.
 PS Claim 1: Page 1209-1211; 1409pp: English.
 CC The present invention describes a computer readable medium which has
 CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
 CC on it, or a representative fragment or a sequence at least 95% identical
 CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
 CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus
 CC pneumoniae. The present invention also describes an isolated nucleic acid

CC molecule encoding a homologue of any of the fragments of the S pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 3902 BP; 1138 A; 714 C; 834 G; 1216 T;

Query Match 66.7%; Score 18; DB 1; Length 3902;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGCTGCAGATTTCGTCTATCTC 27
DB 1286 GGCTCCGACTTTTGTGCGATCTC 1261
||||| ||||| ||||| ||||| |||||

RESULT 6
V65242/c
ID V65242 standard; DNA; 3189 BP.
AC V65242:
DT 24-DEC-1998 (first entry)
DE DNA encoding three S. pneumoniae proteins with different functions.
KW Streptococcus pneumoniae protein; recombinant; gene expression;
KW DNA chip; virulence; antibody; infection; detection; treatment; ss.
OS Streptococcus pneumoniae.
PN WO9826072-21.
PD 18-JUN-1998.
PF 09-DEC-1997; U22578.
PR 13-DEC-1996; US-036281.
PA (ELIL) LILLY & CO ELI.
PI Balazs RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR,
PI Mills RJ, Norris FH, Peery RB, Rostock PR,
PI Skatrud PL, Smith MC, Solenberg FU, Treadway FU,
PI Young Belindo ML;
DR WPI: 98-348529/30.
DR P-PSDB: W80666, W80667, W80668.
DR Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
PT genes
PS Claim 1; Pages 94-96; 333p; English.
CC This DNA encodes S. pneumoniae nitrate reduction, formate dependent
CC protein, lacpressor and a nucleotide reductase. The invention provides
CC DNA sequences (V65201 to V65304) from the S. pneumoniae genome and
CC corresponding protein sequences (W80605 to W80728). A recombinant host
CC containing a vector comprising any of the above nucleic acids can be used
CC for the recombinant expression of the protein sequences. The invention
CC also provides a DNA chip having arrayed on it at least 15 base pair
CC fragment of any one or more of these DNA sequences. The DNA chip can be
CC used methods for evaluating gene expression in S. pneumoniae and for
CC identifying virulence genes in S. pneumoniae. Antibodies that selectively
CC bind to the above proteins or peptide fragments can be used to treat
CC S. pneumoniae infection. The antibodies can also be used to detect
CC S. pneumoniae cells.
SQ Sequence 3189 BP; 956 A; 547 C; 615 G; 1071 T;

Query Match 66.7%; Score 18; DB 1; Length 3189;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGCTGCAGATTTCGTCTATCTC 27

DB 2743 GGCTCCGACTTTTGTGCGATCTC 2718
||||| ||||| ||||| ||||| |||||

RESULT 7
T40119
ID T40119 standard; DNA; 1524 BP.
AC T40119;
DT 28-JAN-1997 (first entry)
DE Human papillomavirus type 18 L1 capsid protein gene.
KW HPV-18; L1 gene; capsid protein; vaccine; diagnosis; vector;
KW antibody; serotyping; cervix carcinoma; ss.
OS Human papillomavirus type 18.
PN WO9629413-A2.
PD 26-SEP-1996.
PF 18-MAR-1996; U03649.
PR 22-MAR-1995; US-409122.
PR 22-MAR-1995; US-408669.
PA (MERI) MERCK & CO INC.
PI George HA, Hofmann KU, Jansen KU, Joyce JC, Neepier MP;
PI WPI: 96-443188/44.
DR P-PSDB: W05843.
PT DNA encoding human papilloma virus 18, esp. L1 and L2 capsid
PT proteins - and related vectors and antibodies, useful in protective
PT vaccines, for serotyping HPV infections and as therapeutic agents
PS Claim 2; Fig 1; 46pp; English.
CC The L1 gene (T40119) codes for the major capsid protein (W05843) of
CC human papillomavirus type 18 (HPV18), an HPV type associated with
CC invasive carcinomas of the cervix, vagina, vulva and anal canal.
CC The DNA sequence was deduced from a genomic clone isolated from
CC human cervical carcinoma-derived SW756 cells using an HPV18 L1
CC probe. The HPV18 L1 and L2 (see also T40120) genes can be used
CC in vaccines against HPV18 infection, as probes, or to produce
CC recombinant capsid proteins in host cells.
SQ Sequence 1524 BP; 396 A; 292 C; 337 G; 499 T;

Query Match 65.2%; Score 17.6; DB 1; Length 1524;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 CTGCAGATTTCGTCTATCTC 27
DB 1154 CTGCAGATTTCGTCTATCTC 1177
||||| ||||| ||||| ||||| |||||

RESULT 8
T91248
ID T91248 standard; DNA; 455 BP.
AC T91248;
DT 24-APR-1998 (first entry)
DE Human papilloma virus HPV-18 DNA sequence for generating probes.
KW Human papilloma virus; HPV; probe; isolation; detection; hybridise; ds.
OS Human papillomavirus
FH Key Location/Qualifiers
FT 1..21
FT misc_feature
FT 1..67
FT /note="Claimed probe for HPV-18"
FT 25..67
FT /tag="b"
FT /note="Claimed probe for HPV-18"
FT 70..119
FT /tag="c"
FT /note="Claimed probe for HPV-18"
FT 121..139
FT /tag="d"
FT /note="Claimed probe for HPV-18"
FT 163..191
FT /tag="e"
FT /note="Claimed probe for HPV-18"
FT 193..284
FT /tag="f"
FT /note="Claimed probe for HPV-18"

AC 053212;
 DT 22-JUN-1994 (first entry)
 DE Human cyclin D3 promoter.
 KW D-type; mammalian; CLN protein; protein deficiency; cell cycle start;
 OS Homo sapiens.
 FT misc_feature
 FT 3156..3158
 FT /tag- a
 FT /note= "Initiation ATG codon"
 PN WO9324514-A.
 PD 09-DEC-1993.
 PE 25-MAY-1993: U05000.
 PR 26-MAY-1992: US-888178.
 PA (MITO-) MITOTIX.
 PI Besch DH;
 DR WPI: 93-405720/50.
 PT New D-type mammalian cyclin - replaces CLN-type protein needed
 PT for cell start in budding yeast and is detected by antibodies or
 PT hybridisation in biological samples to determine abnormal cell
 PT division
 PS Disclosure: Fig 13, 108pp: English.
 CC The sequence is that of human cyclin D3 promoter.
 CC Sequence 3158 BP: 952 A; 674 C; 722 G; 810 T;
 SQ

Query Match 63.0%; Score 17; DB 1; Length 3158;
 Best Local Similarity 80.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGCGTCGAGATTCTGCTATAC 25
 | ||||| ||||| ||||| ||
 DB 2498 TTGCTCGAGATTCTGCTATAC 2474

RESULT 12
 067458
 ID 067458 standard; cDNA to RNA; 2088 BP.
 AC 067458;
 DT 21-APR-1995 (first entry)
 DE Codes tau-protein kinase I (TPK-I), Alzheimer's disease.
 KW Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease; ds.
 OS Homo sapiens.
 FT Key
 FT mat_peptide
 FT 616..1885
 FT /tag- a
 PN EP-616032-A.
 PD 21-SEP-1994.
 PE 01-MAR-1994: 103057.
 PR 02-MAR-1993: JP-041160.
 PR 22-MAR-1993: JP-085143.
 PR 02-AUG-1993: JP-191246.
 PA (TAKA/) TAKASHIMA A.
 PA (MITU) MITSUBISHI KASEI CORP.
 PI Hoshino T, Imahori K, Saito S, Shirauchi A;
 PI Takashima A;
 DR WPI: 94-287181/36.
 DR P-PSD; R61326.
 PT Newly isolated tau-protein kinase I enzyme - with specificity for
 PT tau-protein providing means for prevention and treatment of
 PT Alzheimer's disease
 PS claim 4: Page 14; / English.
 CC 067458 codes for a newly isolated tau-protein kinase I enzyme
 CC (TPK-I), shown in R61326 (compare to rat R61327). The cDNA
 CC was cloned from a rat fetus brain cDNA library, and was expressed
 CC in insect cells. TPK-I acts specifically on tau-protein, which is
 CC thought to be involved in Alzheimer's disease (AD) and senile
 CC dementia of the AD type. It is hoped that the characterisation of
 CC TPK-I may lead to development of new agents for the prevention
 CC and therapy of these diseases.
 CC Sequence 2088 BP: 656 A; 452 C; 434 G; 546 T;
 SQ

Query Match 63.0%; Score 17; DB 1; Length 2088;
 Best Local Similarity 80.0%; Pred. No. 37;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGCGTCGAGATTCTGCTATAC 25
 | ||||| ||||| ||||| ||
 DB 536 TGCGTCGAGATTCTGCTATAC 560

RESULT 13
 T85540
 ID T85540 standard; DNA; 387 BP.
 AC T85540;
 DT 14-APR-1998 (first entry)
 DE gp32 (opt) synthetic gene segment.
 KW Human; tissue-specific plasmidogen activator; tpa; leader; vaccine;
 KW infection; HIV; env; human immunodeficiency virus; PCR primer; ss.
 OS Synthetic.
 OS Human immunodeficiency virus.
 PN WO9731115-A2.
 PD 28-AUG-1997.
 PE 18-FEB-1997: U02294.
 PR 09-APR-1996: GB-007293.
 PR 22-FEB-1996: US-012082.
 PA (MERT) MERCK & CO INC.
 PI Davies M, Freed DC, Liu MA, Perry HC, Silver JW;
 DR WPI: 97-433167/40.
 PT Synthetic DNA encoding HIV env protein - comprises codon(s)
 PT optimised for expression in mammalian host, useful as vaccine
 PT against infection
 PS Example 11: Page 57: 82pp: English.
 CC The present specification describes a synthetic DNA sequence encoding
 CC human immunodeficiency virus (HIV) env protein, or a fragment,
 CC comprising codons optimised for expression in a mammalian host. The
 CC present sequence represents a synthetic gene segment from an example of
 CC the present invention. The new synthetic DNA sequence induces anti-HIV
 CC neutralising antibody, HIV specific T cell immune responses, or
 CC protective immune responses upon introduction into vertebrate tissue,
 CC including human tissue in vivo, where the DNA comprises a gene encoding
 CC a HIV gag, gag protease or env gene product. The DNA can also be used
 CC to induce an immune response against infection or disease caused by
 CC virulent strains of HIV, optionally in conjunction with attenuated HIV,
 CC killed HIV or HIV env, gag or pol protein, or to induce an anti-HIV
 CC response in a primate when administered parenterally in conjunction
 CC with interleukin 12. The new DNA can also be used to induce an antigen
 CC presenting cell to stimulate cytotoxic and helper T cell proliferation
 CC and effector functions, including lymphokine secretion specific to HIV
 CC antigens, by expressing vertebrate cells to it in vivo, or as a vaccine
 CC against HIV infection. The codons of new synthetic DNA are designed so
 CC as to use the codons preferred by the projected host cell.
 CC Sequence 387 BP: 91 A; 102 C; 113 G; 81 T;
 SQ

Query Match 63.0%; Score 17; DB 1; Length 387;
 Best Local Similarity 80.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGCTGCGAGATTCTGCTATAC 26
 | ||||| ||||| ||||| ||
 DB 306 GGCTGCGAGATTCTGCTATAC 330

RESULT 14
 V21766
 ID V21766 standard; DNA; 387 BP.
 AC V21766;
 DT 20-JUL-1998 (first entry)
 DE HIV gp32 (opt) gene segment from AVRII site.
 KW Vlnuo; HIV vaccine; codon usage optimisation; HIV; immune response;
 KW human immunodeficiency virus; hepatitis; tuberculosis; tumour;
 KW env protein; gp32; recombinant; ss.
 OS Synthetic.
 OS Human immunodeficiency virus.

PN MO9748370-A2.
 PD 24-DEC-1997.
 PF 17-JUN-1997: U10517.
 PR 16-JUL-1996: GB-014943.
 PR 21-JUN-1996: US-020165.
 PR 21-JUN-1996: US-020166.
 PR 16-JUL-1996: GB-014942.
 PA (MERI) MERCK & CO INC.
 PI Davies ME, Freed DC, Liu MA, Perry HC, Silver JW;
 DR MPI: 98-062825/06.
 PT DNA encoding protein with codon usage optimised for intended host
 PT cell - specifically for DNA vaccines against human immune deficiency
 PT virus, allows rev-independent expression of HIV genes
 PS Example 11: Pages 54-55; 113pp: English.
 CC This is a HIV gp12 gene segment from the Avrii site to the end of gp143
 CC having optimal codon usage (Opt) for expression. This can be used in an
 CC expression vector for vaccine production. The expression vector contains
 CC a new synthetic DNA, encoding a HIV env protein or its fragment and has
 CC codons optimised for expression in a non-homologous host. The synthetic
 CC DNA sequences are used to increase production of recombinant protein and
 CC to induce anti-HIV neutralising antibody, HIV-specific T-cell immune
 CC responses or protective immune responses in vertebrates, specifically as
 CC HIV vaccines. Optimisation of codons results in increased expression of
 CC the DNA in the host. The DNA induces antigen-presenting cells to
 CC stimulate cytotoxic and helper T-cells, and effector functions such as
 CC lymphokine secretion specific to HIV antigens. Cross-strain protection is
 CC achieved without use of adjuvant and the synthetic DNA may provide a
 CC longer-lasting response. The env gene includes a high proportion of
 CC codons rarely used in mammals, so optimisation will allow this gene to
 CC be expressed efficiently in absence of rev. The DNA sequences, more to
 CC generally, may express antigens from many other pathogens, e.g. hepatitis
 CC or tuberculosis, and also from tumours.
 SQ Sequence 387 BP; 91 A; 102 C; 113 G; 81 T;

Query Match 63.0%; Score 17; DB 1; Length 387;
 Best Local Similarity 80.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGCTGCAGATTTCGTGCTACT 26
 ||||| |||| |||| ||||
 Db 306 GGCTGCAGATTTCGTGCTACT 330

RESULT 15
 T80646/C
 ID T80646 standard: DNA; 422 BP.
 AC T80646:
 DT 11-NOV-1997 (first entry)
 DE Type II topoisomerase database reference sequence SEQ ID NO:59.
 KW Detection; Identification; TopoII; contamination; food; human;
 KW animal; plant; soil; water; PCR; polymerase chain reaction; ds.
 OS Chlamydia trachomatis.
 PN US5645994-A.
 PD 08-JUL-1997.
 PF 05-JUL-1990: 548138.
 PR 06-JUN-1995: US-470179.
 PR 05-JUL-1990: US-548138.
 PR 13-AUG-1993: US-106482.
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Huang NM;
 DR MPI: 97-362925/33.
 PT Detection and identification of organisms - using DNA primers to
 PT amplify signature segment of organism's type II topoisomerase
 PS Claim 6: Column 71-72; 114pp: English.
 CC A method has been produced for selectively amplifying DNA segments of
 CC one or more species of organisms in a sample. The method involves: (a)
 CC providing a database containing reference sequences, comprising a
 CC subunit sequence of a signature region of a macromolecule selected from
 CC a type II topoisomerase (TopoII), or a homologue, where each reference
 CC sequence is specific to a different species of a chosen group, and the
 CC macromolecule comprises 1st and 2nd conserved regions adjacently
 CC flanking the signature region; and (b) making an extract of DNA

CC molecules, and selectively amplifying DNA segments of the signature
 CC region using a universal primer composition, comprising a primer
 CC constructed to bind a DNA encoding the macromolecule, to produce
 CC amplified DNA segments. The present sequence represents a DNA fragment
 CC containing a signature segment which is used in the database as a
 CC reference sequence for Chlamydia trachomatis. The method can be used
 CC to identify all of the different organisms present in a single
 CC sample without using multiple probes. It can accurately distinguish
 CC among similar and related species, and can be used with, e.g.
 CC contaminated food products, tissue or fluid samples from diseased
 CC humans, animal or plants, soil samples and water samples from any
 CC source.
 SQ Sequence 422 BP; 121 A; 90 C; 93 G; 118 T;

Query Match 61.5%; Score 16.6; DB 1; Length 422;
 Best Local Similarity 82.6%; Pred. No. 42;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCAGATTTCGTGCTACTC 27
 ||| ||||| ||||| ||||
 Db 87 TGCAGATTTCGTGCTACTC 65

Search completed: July 15, 1999, 00:27:46
 Job time: 7699 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 1999, 00:27:39 ; Search time 269.22 seconds

(without alignments)
19.566 Million cell updates/sec

Title: US-08-943-144-8

Perfect score: 28
Sequence: 1 GATTGCTGAACACAAAGATATGCTAAT 28

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	4412	1 V40710	Aldehyde oxidase g
2	28	100.0	28	1 V40715	Primer for aldehyd
3	20	71.4	4689	1 O54386	T. niveum Cyclospo
4	19	67.9	5181	1 O80911	Plasmodium falcipa
5	18.8	67.1	1463	1 V61483	Human secreted pro
6	18.4	65.7	2153	1 O06168	Encodes Human Bone
7	18.4	65.7	2153	1 O32854	BMP5. Synergistic
8	18.4	65.7	2153	1 O41295	Human BMP-5 gene.
9	18.2	65.0	3658	1 T31202	Prb1 gene encoding
10	18	64.3	1593	1 T86242	CDNA for birch pol
11	18	64.3	5053	1 V21209	CDNA of protein w1
12	17.8	63.6	110000	1 V21209_14	Continuation (15 o
13	17.6	62.9	4363	1 V23128	Vicilin signal pep
14	17.6	62.9	4359	1 V40711	CDNA of protein w1
15	17.6	62.9	4359	1 V40711	Aldehyde oxidase g
16	17.4	62.1	133894	1 T13635	Primer for aldehyd
17	17.4	62.1	133894	1 T13635	Acnrv genomic DNA
18	17.4	62.1	80073	1 T58840_5	Acnrv ORF 92, resi
19	17.4	62.1	80073	1 T58840_5	Continuation (6 of
20	17.2	61.4	255	1 T94201	ARP.3 endoglucana
21	17	60.7	4410	1 O93913	Yeast MSH1 gene. D
22	17	60.7	110000	1 V21209_00	Methanococcus jann
23	16.8	60.0	4868	1 O23679	Encodes Human BMP-
24	16.8	60.0	4868	1 V26068	Human canalicular
25	16.8	60.0	3323	1 T84223	DNA encoding a glu
26	16.8	60.0	7313	1 V29268	Nucleotide sequenc
27	16.8	60.0	3323	1 V53546	DNA encoding 2 Sta
28	16.8	60.0	110000	1 V21209_02	Continuation (3 of
29	16.6	59.3	397	1 O59285	Expressed Sequence
30	16.6	59.3	397	1 O59285	Human brain expres
31	16.4	58.6	1085	1 O04703	Legumin-signalpep
32	16.4	58.6	2844	1 N71250	Sequence of Vicia
33	16.4	58.6	5499	1 O31189	Alpha 6B integrin
34	16.4	58.6	5629	1 O31188	Alpha 6A integrin
35	16.4	58.6	1200	1 O52267	zPDS.1711 DNA. Con
36	16.4	58.6	5529	1 O65673	Sequence encoding
37	16.4	58.6	1207	1 T26894	Sequence encoding
38	16.4	58.6	225	1 T25137	Bacteriophage resi
39	16.4	58.6	2457	1 T30736	Human gene signatu
40	16.4	58.6	1239	1 T68012	Rat cryptidin 1 gen
41	16.4	58.6	309	1 T67833	H. pylori secreted
42	16.4	58.6	309	1 T77513	H. pylori secreted
43	16.4	58.6	309	1 T77513	H. pylori secreted

C 44 16.4 58.6 1131 1 V12775
45 10.4 58.6 1450 1 V16886

Metal-regulated tr
Human prostate can

ALIGNMENTS

RESULT 1

V40710 ID V40710 standard; CDNA to mRNA; 4412 BP.

AC V40710; DT 22-SEP-1998 (first entry)

DE Aldehyde oxidase gene.

KM Aldehyde oxidase; auxin production; plant maturation; ss.

OS Zea mays.

FH Key Location/Qualifiers

FT CDS 46..4122

PI WPT: 98-195460/18.

DR P-PSDB; W57837.

PT Aldehyde oxidase gene from plants and related vector and transformed

PS Claim 3: Page 17-21; 34pp: English.

CC This sequence encodes the Zea mays aldehyde oxidase protein of the

CC Invention. The enzyme is able to oxidise an aldehyde to carboxylic acid

CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells

CC transformed with the DNA are used to express the enzyme. Specifically

CC expression of the DNA in transformed plants is used to increase (or

CC suppress) production and activity of auxin, e.g. to cause earlier

CC maturation of crops, improved yields and quality of fruit, to prevent

CC weak growth, to develop strains able to grow under suboptimal conditions,

CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten

CC flowers. Also plant cells that over-express the DNA can be proliferated,

CC differentiated and regenerated in sterile medium, particularly for

CC production of virus-free nursery stock (of flowers or ornamental plants).

CC Sequence 4412 BP; 1193 A; 1061 C; 1142 G; 1016 T;

CC Query Match 100.0%; Score 28; DB 1; Length 4412;

CC Best Local Similarity 100.0%; Pred. No. 0.0016;

CC Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 GATTGCTGAACACAAAGATATGCTAAT 28

CC DB 2100 GATTGCTGAACACAAAGATATGCTAAT 2127

CC RESULT 2

V40715 ID V40715 standard; DNA; 28 BP.

AC V40715; DT 22-SEP-1998 (first entry)

DE Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.

KM Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.

OS Zea mays.

PN EP-834558-A2.

PD 08-APR-1998.

PF 02-OCT-1997; 117168.

PR 04-OCT-1996; JP-28314.

PA (SUMO) SUMITOMO CHEM CO LTD.

PI Koshida T.

DR WPT: 98-195460/18.

PT Aldehyde oxidase gene from plants and related vector and transformed

PT cells - particularly for modulating auxin production in plants to

PT accelerate maturation, increase yield, induce dwarfing etc.

PS Example 8; Page 7; 34pp; English.
 CC This sequence represents a primer for the DNA encoding the Zea mays
 CC aldehyde oxidase protein of the invention. The enzyme is able to oxidise
 CC an aldehyde to carboxylic acid (specifically indole acetaldehyde to
 CC indole acetic acid (auxin). Cells transformed with the DNA are used to
 CC express the enzyme. Specifically expression of the DNA in transformed
 CC plants is used to increase (or suppress) production and activity of
 CC auxin, e.g. to cause earlier maturation of crops, improved yields and
 CC quality of fruit, to prevent weak growth, to develop strains able to grow
 CC under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging
 CC in rice) and to shorten flowers. Also plant cells that over-express the
 CC DNA can be proliferated, differentiated and regenerated in sterile
 CC medium, particularly for production of virus-free nursery stock (of
 CC flowers or ornamental plants).
 SQ Sequence 28 BP; 12 A; 4 C; 5 G; 7 T;

Query Match 100.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GATTGCTGAACACAAAGATATGCTAAT 28
 DB 1 GATTGCTGAACACAAAGATATGCTAAT 28

RESULT 3
 ID 054386 standard; DNA; 46899 BP.

AC 054386;
 DT 08-JUL-1994 (first entry)
 DE T. niveum Cyclosporin synthetase gene.
 KW Enzyme: cyclosporin; synthetase-like activity; Tolypocladium niveum;
 KM T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase; ss.
 OS Tolypocladium niveum.
 FH Key
 FT cds Location/Qualifiers
 FT 885..46730
 FT /tag= a
 FT /product= Cyclosporin synthetase
 FT 40239..43129
 FT /tag= b
 FT /note= "Salt restriction fragment, preferred
 FT fragment, Claim 4"
 FT 37781..40244
 FT /tag= d
 FT /note= "Salt restriction fragment, preferred
 FT fragment, Claim 5"
 FT misc-feature
 FT 46899 BP;
 PN EP-578616-A.
 PD 12-JAN-1994.
 PF 05-JUL-1993; 810474.
 PR 09-JUL-1992; AT-001403.
 PR 08-MAR-1993; AT-000437.
 PR 29-APR-1993; CH-001310.
 PR 04-MAY-1993; CH-001375.
 PA (SANO) SANDOZ LTD.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERN GES MBH.
 PI Leitner E, Schneider E, Schoergerdorfer K, Weber G;
 DR WPI: 94-010432/02.
 DR P-P50B; R44925.
 PT Isolated DNA sequence - which codes for enzyme having cyclosporin
 PT synthetase like activity
 PS Claim 6; Page 17-41; 93pp; English.
 CC This sequence encodes an enzyme which has cyclosporin synthetase-
 CC like activity. This sequence was isolated from Tolypocladium niveum
 CC (formerly known as T. inflatum GAMS). The enzyme encoded by this
 CC sequence catalyses the peptide biosynthesis of cyclosporins and
 CC structurally related molecules. This sequence may be used for the
 CC production of cyclosporin by transforming a vector containing this
 CC sequence in to a recombinant host. This allows effective production
 CC of antibiotic cyclosporin or its derivatives.
 SQ Sequence 46899 BP; 10651 A; 13513 C; 12509 G; 10226 T;

Query Match 71.4%; Score 20; DB 1; Length 46899;
 Best Local Similarity 82.1%; Pred. No. 5.7;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GATTGCTGAACACAAAGATATGCTAAT 28
 DB 6518 GATTGCTGAACACAAAGATATGCTAAT 6545

RESULT 4

ID 080911 standard; cDNA; 5181 BP.
 AC 080911;
 DT 24-AUG-1995 (first entry)
 DE Plasmodium falciparum MSA-1 gene cDNA.
 KW Plasmodium falciparum MSA-1 gene; recombinant poxvirus;
 KM multicomponent multistage malarial vaccines; immunogens;
 OS malaria diagnosis; ss.
 OS Plasmodium falciparum (p486195).
 PN W09428930-A.
 PD 22-DEC-1994.
 PF 10-JUN-1994; U06652.
 PR 11-JUN-1993; US-075783.
 PR 09-JUN-1994; US-257073.
 PA (VIRO-) VIROGENETICS CORP.
 PI De Taisne C, Paolletti E, Tine JA;
 DR WPI: 95-036113/05.
 PT Recombinant poxvirus contg. Plasmodium DNA in non-essential
 PT region - useful in vaccines against malaria and for prodn. of
 PT Plasmodium immunogens
 PS Claim 3; Fig 6; 183pp; English.
 CC 080911 is the P. falciparum MSA-1 gene cDNA sequence. New
 CC recombinant poxviruses containing either the SERA, ABRA, Pfhp70,
 CC AMA-1, PfS25, PfS16, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1,
 CC MSA-1 (N-terminal p83 or C-terminal gp42) genes, or a combination
 CC of these in non-essential regions of their genomes are claimed.
 CC These poxviruses (pref. with a virulence reducing genomic
 CC deletion or disruption) can be used as vaccines against malaria
 CC and for the prodn. of Plasmodium immunogens. These viruses
 CC provide multicomponent, multistage vaccines due to their expression
 CC of sporozoite, liver stage, blood stage and sexual stage proteins.
 SQ Sequence 5181 BP; 2287 A; 684 C; 707 G; 1503 T;

Query Match 67.9%; Score 19; DB 1; Length 5181;
 Best Local Similarity 81.5%; Pred. No. 11;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 ATTGCTGAACACAAAGATATGCTAAT 28
 DB 1657 AATTGCTGAACACAAAGATATATTAAT 1683

RESULT 5

ID V61483/c standard; cDNA; 1463 BP.
 AC V61483;
 DT 11-JAN-1999 (first entry)
 DE Human secreted protein dn740_3 cDNA.
 KW Secreted protein; human; dn740_3; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 506..1099
 FT /tag= a
 PN W09841539-A2.
 PD 24-SEP-1998.
 PF 19-MAR-1998; U05474.
 PF 18-MAR-1998; US-040963.
 PR 19-MAR-1997; US-820493.
 PA (GENM) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Werberg D,
 PI Racie LA, Spaulding V, Treacy M;

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DR      MPI: 98-521163/44.
DR      New polynucleotide(s) encoding secreted human proteins - derived
PT      from human foetal Kidney, adult testes and adult or foetal Brain
PT      cDNA libraries
PS      Claim 24: Page 78-79: 112pp: English.
CC      This full-length cDNA clone, designated dn740.3, codes for a novel
CC      secreted human protein (see w79092). It was isolated from a human
CC      foetal brain cDNA library using methods which are selective for
CC      cDNAs encoding secreted proteins, or was identified as encoding
CC      a secreted or transmembrane protein on the basis of computer
CC      analysis of the encoding protein. The nucleotide sequence shows
CC      homology to some database sequences, and may contain a simple AT
CC      repeat sequence. The invention provides cDNA clones (see
CC      W61477-87) from human foetal Kidney, adult testis, and adult or
CC      foetal brain cDNA libraries that code for secreted proteins (see
CC      w79087-97). These clones are deposited as ATCC 98364. The
CC      polynucleotides and proteins are predicted to be useful
CC      biological activities which would make them suitable for treating,
CC      preventing or ameliorating medical conditions in humans and
CC      animals, although no supporting data is given. Suggested
CC      activities include nutritional, immune stimulating (e.g. as
CC      vaccines) or suppressing, haematopoiesis regulating, tissue growth,
CC      activin/inhibin, chemotactic/chemokinetic, haemostatic and
CC      thrombolytic, receptor/ligand, antiinflammatory, cachectic/tumour
CC      invasion suppressor and tumour inhibition activities. The
CC      polynucleotides are also stated to be useful for gene therapy.
SQ      Sequence 1463 BP; 360 A; 408 C; 385 G; 310 T;

Query Match          67.1%; Score 18.8; DB 1; Length 1463;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Oy      7 TGAACACAAAGATATGCTAAT 28
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      1340 TAAAGCACAAAGATATGCTAAT 1319

RESULT 6
ID      006168/c
AC      006168 standard; DNA; 2153 BP.
DI      30-JAN-1991 (first entry)
DE      Encodes Human Bone Morphogenic Protein (BMP)-5.
KW      human bone morphogenic protein-5; wound healing; tissue repair;
        cartilage formation; ss.
OS      Homo sapiens.
FH      Key Location/Qualifiers
FT      cds 701..2063
FT      FT /tag= a
FT      FT /product=BMP-5 precursor
FT      FT 1..700
FT      FT 5'utr /tag= b
FT      FT 2064..2153
FT      FT 3'utr /tag= c
FT      FT
PN      WO9011366-A.
PD      04-OCT-1990.
PE      27-MAR-1990: U01630.
PR      28-MAR-1989: US-329610.
PR      04-MAY-1988: US-347559.
PR      23-JUN-1989: US-370547.
PR      23-JUN-1989: US-370544.
PR      15-NOV-1989: US-437409.
PR      17-NOV-1989: US-438919.
PR      07-MAR-1990: US-440033.
PA      (GENE-) GENETICS INST INC.
PI      Wang EA, Moznay JM, Celeste AJ:
DR      P-PSDB: R07310.
PT      New bone morphogenic proteins, BMP-5, -6 and -7 - used for
PT      stimulating, promoting and inducing bone and/or cartilage

```

PT	formation, wound healing and tissue repair
PS	Example; Page 45; 96pp; English.
CC	A cDNA library was made in the vector lambda ZAP from human
CC	osteosarcoma cell line U-20S poly(A)-contg. RNA. 750,000 recombinants
CC	were plated and nitrocellulose duplicates made and screened. The
CC	probes are based on the sequence of fragments of bovine BMP-6 and
CC	BMP-5. 17 clones were found to bind more strongly to the BMP-5 probe.
CC	One of the clones, U2-16, was sequenced and contained a fragment with
CC	the sequence given here.
CC	See also Q06166, Q06167, Q06169-Q06173, Q06187-Q06192.
SO	Sequence 2153 BP; 703 A; 420 C; 450 G; 580 T;
QY	1 GATTGCTGAACACAAAGATATGCGAAT 28
DB	
DB	240 GATTTCGTCAATCAGATCTATGCTGAT 213
RESULT 7	
ID	Q32854/c
AC	Q32854; standard; cDNA; 2153 BP.
DT	05-MAY-1993 (first entry)
DE	BMP5.
KW	Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
OS	treatment; dimer; ss.
PN	WO9221365-A.
PD	10-DEC-1992.
PF	26-MAY-1992; U04356.
PR	05-JUN-1991; US-709621.
PR	27-MAR-1992; US-856110.
PA	(PROC) PROCTER & GAMBLE CO.
PI	Stone RL;
PI	WPI: 92-43371/52.
PT	Synergistic compsn. for generating mammalian bone growth -
PT	comprises vitamin-D cpd. and bone morphogenetic protein
PS	Disclosure; Page 33-34; 44pp; English.
CC	The sequences given in Q32850-56 encode bone morphogenetic proteins
CC	(BMP). BMP's increase bone growth and when used in conjunction with
CC	vitamin D the level of new bone growth is greater than when a BMP or
CC	vitamin D are used alone. The BMP's are administered for systemic
CC	treatment at a dose range of 1pg to 100 microg. BMP are active as
CC	dimers.
SO	Sequence 2153 BP; 703 A; 420 C; 450 G; 580 T;
Query Match	65.7%; Score 18.4; DB 1; Length 2153;
Best Local Similarity	78.6%; Pred. No. 18;
Matches 22; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
QY	1 GATTGCTGAACACAAAGATATGCTAAT 28
DB	
DB	240 GATTTCGTCAATCAGATCTATGCTGAT 213
RESULT 8	
ID	Q41295/c
AC	Q41295; standard; DNA; 2153 BP.
DT	13-SEP-1993 (first entry)
DE	Human BMP-5 gene.
KW	Bone morphogenetic protein; bone defect treatment; healing; wound;
KW	injury; tissue repair; osteoporosis; burns; incisions; ulcers;
KW	neuronal survival increase; fracture reduction; cartilage growth;
OS	induction; ss.
OS	Homo sapiens.
FN	Key
FT	cds
FT	Location/Qualifiers
FT	699..2063

```

FT      mat_peptide      /tag- a
FT      1647. 2060
FT      /tag- b
FT      1. 2153
FT      /tag- c
PN      WO9309229-A.
PD      13-MAY-1993.
PR      02-NOV-1992. 009430.
PR      04-NOV-1991. US-787496.
PR      07-APR-1992. US-864692.
PA      (GEM) GENETICS INST INC.
PI      Israel D. Wolfman NM;
PI      WPI: 93-167696/20.
DR      P-PSDB: R36736.
PT      Recombinant hetero-dimeric BMP proteins - are useful in treating
PS      bone defects, healing bone injury and in wound healing
PS      disclosure; Fig 5: 16pp; English.
CC      The sequence is that encoding the human bone morphogenetic protein
CC      BMP-5. It may be used in the prodn. of a recombinant heterodimeric
CC      protein having bone stimulating activity. This heterodimer is
CC      encoded by a sequence encoding BMP-2 or BMP-4 or a fragment and a
CC      sequence encoding a second protein or fragment, BMP-5. It may be
CC      used in compns. for wound healing, tissue repair, and in similar
CC      compns. which have been indicated for the use of individual BMPs.
CC      Increased potency of the heterodimer over individual BMPs may permit
CC      lower dosages to be administered. A heterodimeric protein which
CC      induces cartilage and/or bone growth in circumstances where bone
CC      is not normally formed, has applications in the healing of bone
CC      fractures and cartilage defects in humans and other animals. The
CC      heterodimer may have prophylactic use in closed as well as open
CC      fracture reduction and also in the improved fixation of artificial
CC      joints. De novo bone formation induced by an osteogenic agent
CC      contributes to the repair of congenital, trauma induced or oncologic
CC      resection induced craniofacial defects, and also is useful in cosmetic
CC      plastic surgery. It may be used in the treatment of periodontal
CC      disease and in other tooth repair processes. It may also be useful
CC      in the treatment of osteoporosis, wound healing (e.g. burns,
CC      incisions and ulcers) and related tissue repair, and may increase
CC      neuronal survival and be useful in the transplantation and treatment
CC      of conditions exhibiting a decrease in neuronal survival. It may be
CC      combined with other agents beneficial to the bone and/or cartilage
CC      defect, wound or tissue in question, e.g. EGF, PDGF, TGF-alpha,
CC      TGF-beta and insulin-like growth factor
CC      Sequence 2153 BP; 703 A; 422 C; 448 G; 580 T;
SQ

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Query Match 65.7%; Score 18.4; DB 1; Length 2153;
 Best Local Similarity 78.6%; Pred. No. 18;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY      1 GATTGCTGAACACAAAGATATGCTAT 28
      ||||| ||||| ||||| ||||| ||
DB      240 GATTGCTGAATCACAGATCTATGCTAT 213

```

RESULT 9
 T31202
 ID T31202 standard; DNA: 3668 BP.
 AC T31202;
 DT 17-JAN-1997 (first entry)
 DE Prbl gene encoding protease Prbl.
 KW Prbl; transform: biological control; phytopathogenic fungi; nematode;
 KW Infested soil; transgenic; protease; ss.
 OS Trichoderma harzianum strain IMI 206040.
 PN WO9618722-A2.
 PD 20-JUN-1996.
 PR 08-DEC-1995. MX0009.
 PR 08-DEC-1994. MX-009542.
 PA (INVE-) CENT INVESTIGACION ESTUDIOS AVANZADOS.
 PI Chet I, Flores Martinez A, Herrera Estrella A;
 PI WPI: 96-300641/30.
 DT transformed Trichoderma spp. strain prepn. - by introduction of gene
 coding for proteinase Prbl prodn. which attacks cell walls of fungi

```

PT      and nematodes
PS      Disclosure; Fig 1: 28pp; Spanish.
CC      The present sequence is that of the prbl gene, which encodes Prbl
CC      protease, isolated from Trichoderma harzianum strain IMI 206040.
CC      Direct transformation of Trichoderma spp. with the prbl gene is useful
CC      for producing improved strains of Trichoderma which are useful as
CC      biological control agents. They are esp. useful for control of
CC      phytopathogenic fungi and nematodes in infested soils.
SQ      Sequence 3668 BP; 937 A; 875 C; 812 G; 1044 T;

```

Query Match 65.0%; Score 18.2; DB 1; Length 3668;
 Best Local Similarity 87.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY      1 GATTGCTGAACACAAAGATATG 23
      ||| ||| ||||| ||||| |||||
DB      2797 GATGCTTAACAAAGATATG 2819

```

RESULT 10
 T86242
 ID T86242 standard; cDNA to mRNA: 1593 BP.
 AC T86242;
 DT 07-JAN-1998 (first entry)
 DE cDNA for birch pollen co-factor-independent phosphoglycerate mutase.
 KW Cofactor-independent phosphoglycerate mutase; PGM-1; E.C. 5.4.21.
 KW birch; pollen; allergy; plant allergen; panallergen; B cell;
 KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
 KW conserved; ds.
 OS Betula verrucosa.
 FH Key
 FH Key 1. 1593
 FT CDS
 FT /tag- a
 FT /note- "no start codon given"
 PN MO9705258-A2.
 PD 13-FEB-1997.
 PR 02-AUG-1996. AT0141.
 PR 02-AUG-1995. AT-001320.
 PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
 PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
 PI Kraft D, Richter K, Rheinberger H;
 PI WPI: 97-145695/13.
 DR P-PSDB: W28501.
 PT New recombinant DNA encoding plant phosphoglycerate mutase or its
 PT antigenic epitope(s) - useful for diagnosis or treatment of
 PT allergies to pollen and plant-derived foods
 PS Claim 1, Fig 1: 16pp; German.
 CC T86242 encodes birch pollen co-factor-independent phosphoglycerate
 CC mutase (PGM-1). PGM-1 is a highly conserved plant allergen (panallergen)
 CC which can cause cross-reactivity in patients allergic to pollen and
 CC plant-derived foods. PGM-1 and it's B cell and T cell epitopes can be
 CC used for the in vitro detection of allergy against PGM-1, by measuring
 CC serum IgE or a cellular reaction. They can also be used in immunotherapy
 CC and will not cause an autoimmune response because PGM-1 is significantly
 CC different from the human enzyme, which is co-factor dependent.
 SQ Sequence 1593 BP; 424 A; 301 C; 433 G; 435 T;

Query Match 64.3%; Score 18; DB 1; Length 1593;
 Best Local Similarity 80.8%; Pred. No. 26;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY      1 GATTGCTGAACACAAAGATATGCTA 26
      ||||| ||||| ||| |||||
DB      1128 GATTGCTGAACAAACGAGATGCTA 1153

```

RESULT 11
 V23127
 ID V23127 standard; cDNA: 5053 BP.
 AC V23127;
 DT 14-AUG-1998 (first entry)

DE cDNA of protein with Rho protein-combining and kinase activity.
KM Rho protein-binding activity; protein kinase activity; inhibitor;
KM smooth muscle fibre formation; smooth muscle contraction;
KM circulatory disease; treatment; tumour formation; metastasis inhibitor;
KM autoimmune disease; platelet aggregation inhibitor; ss.

OS Bos sp.
FH Key 1.4167 Location/Qualifiers
FT CDS
FT misc-feature 3889..3936
FT /*tag= a
FT /*tag= b
FT /*note= "the amino acid residues encoded by these
nucleotides do not appear in the protein
sequence"

FT J10113187-A.
PD 06-MAY-1998.
PF 20-NOV-1996; 324594.
PR 23-AUG-1996; JP-241061.
PR 20-NOV-1995; JP-325129.
PR 05-JAN-1996; JP-017150.
PR 26-APR-1996; JP-131206.
PA (KIRI) KIRIN BREWERY KK.
DR WPI: 98-315475/28.
DR P-PDB: W56473.
PT Bovine and human Rho protein-binding protein kinase - used to
develop products for treatment of smooth muscle disorders,
PT circulatory disease, cancer and autoimmune disease.
PS Disclosure: Pages 39-44; 66pp; Japanese.
CC The present sequence encodes a protein that has Rho protein-binding
activity and protein kinase activity. Inhibitors of the Rho-binding
protein kinase can be used to inhibit smooth muscle fibre formation
CC and smooth muscle contraction. Other applications of the Rho
protein-binding agent and its products are as a circulatory disease
CC treating agent, a tumour formation or metastasis inhibitor, an
CC autoimmune disease treating agent or a platelet aggregation inhibitor.
SQ Sequence 5053 BP; 1816 A; 879 C; 1092 G; 1266 T;

Query Match 64.3%; Score 18; DB 1; Length 5053;
Best Local Similarity 80.8%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 ATTGCTGAACACAAAGATGCTAA 27
DB 2331 ACTCTCAACACAAAGATGCTAA 2356

RESULT 12
V21209_14

Continuation (15 of 17) of V21209 from base 1400001 (Methanococcus jannaschii circular c
WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

WP	Fragment Name	Begin	End
WP	V21209_00	1	110000
WP	V21209_01	100001	210000
WP	V21209_02	200001	310000
WP	V21209_03	300001	410000
WP	V21209_04	400001	510000
WP	V21209_05	500001	610000
WP	V21209_06	600001	710000
WP	V21209_07	700001	810000
WP	V21209_08	800001	910000
WP	V21209_09	900001	1010000
WP	V21209_10	1000001	1110000
WP	V21209_11	1100001	1210000
WP	V21209_12	1200001	1310000
WP	V21209_13	1300001	1410000
WP	V21209_14	1400001	1510000
WP	V21209_15	1500001	1610000
WP	V21209_16	1600001	1664976

Query Match 63.6%; Score 17.8; DB 1; Length 110000;
Best Local Similarity 90.5%; Pred. No. 55;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TGAACCAACAAAGATGCTAA 27
DB 17188 TGAACCAACAAAGATGCTAA 17208

RESULT 13
O48744/c
ID O48744 standard; DNA; 45 BP.
AC O48744;
DT 14-MAR-1994 (first entry)
DE Vicilin signal peptide DNA.
KM Vicilin, signal peptide; hybrid protein; resistance; bacteria; fungi;
KM freezing; endoplasmic reticulum; lumen; crop; ss.
OS Pisum sativum.
PN W09318181-A.
PD 16-SEP-1993.
PF 19-FEB-1993; U01494.
PR 13-MAR-1992; US-851429.
PA (CORR) CORNELL RES FOUND INC.
PI Pang S, Sanford JC.
DR WPI: 93-303493/38.
DR P-PDB: R41225.
PT Novel DNA encoding hybrid protein conty. vicilin-derived signal
peptide - useful to transform plant cells to direct a required
PT protein into plants transport system
PS Claim 6; Page 19; 28pp; English.
CC This sequence encodes a vicilin-derived signal peptide. This
CC sequence may be used in the production of a hybrid protein, by
CC fusing it to a second sequence. The second sequence may encode a
CC resistance to bacteria, fungi, or freezing or any other desired
CC effect. This signal peptide enables the hybrid protein to enter the
CC cells transport pathway via the endoplasmic reticulum. Upon entry
CC into the lumen, the signal peptide is cleaved from the second
CC peptide in the same fashion as the vicilin signal peptide would be
CC separated from the vicilin protein to which it is naturally fused.
CC This system may be used to transform virtually any crop plant cell.
SQ Sequence 45 BP; 10 A; 6 C; 7 G; 22 T;

Query Match 62.9%; Score 17.6; DB 1; Length 45;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 TGCTGAACCAACAAAGATGCTAA 27
DB 45 TGATGAACCAACAAAGATGCTAA 22

RESULT 14
V23128
ID V23128 standard; CDNA; 4363 BP.

AC V23128;
DT 14-AUG-1998 (first entry)
DE cDNA of protein with Rho protein-combining and kinase activity.
KM Rho protein-binding activity; protein kinase activity; inhibitor;
KM smooth muscle fibre formation; smooth muscle contraction;
KM circulatory disease; treatment; tumour formation; metastasis inhibitor;
KM autoimmune disease; platelet aggregation inhibitor; ss.
OS Homo sapiens.

FH Key 1.4167 Location/Qualifiers
FT CDS
FT /*tag= a

FT J10113187-A.
PD 06-MAY-1998.
PF 20-NOV-1996; 324594.
PR 23-AUG-1996; JP-241061.
PR 20-NOV-1995; JP-325129.
PR 05-JAN-1996; JP-017150.
PR 26-APR-1996; JP-131206.
PA (KIRI) KIRIN BREWERY KK.
DR WPI: 98-315475/28.

DR P-PSDB: M56475.
PT Bovine and human Rho protein-binding protein kinase - used to develop products for treatment of smooth muscle disorders, circulatory disease, cancer and autoimmune disease.
PS Disclosure: Pages 48-53; 66pp; Japanese.
CC The present sequence encodes a protein that has Rho protein-binding activity and protein kinase activity. Inhibitors of the Rho-binding protein kinase can be used to inhibit smooth muscle fibre formation and smooth muscle contraction. Other applications of the Rho protein-binding agent and its' products are as a circulatory disease treating agent, a tumour formation or metastasis inhibitor, an autoimmune disease treating agent or a platelet aggregation inhibitor
SO Sequence 4363 BP, 1587 A, 769 C, 990 G, 1017 T.

Query Match	62.9%	Score 17.6	DB 1	Length 4363
Best Local Similarity	83.3%	Pred. No. 44		
Matches 20	Conservative	0	Mismatches 4	Indels 0
Gaps				0

OY	4	TGCTGAACACCAAGATGCTTA	27
Db	2333	TCCTTAACAGAAAGATGCTTA	2356

RESULT 15

ID	V40711:standard; cDNA to mRNA; 4359 BP.
DT	22-SEP-1998 (first entry)
DE	Aldehyde oxidase gene.
KW	Aldehyde oxidase; auxin production; plant maturation; ss.
OS	Zea mays.
FT	Key
FT	Location/Qualifiers
FT	91..4140
FT	/*tag= a
PN	EP-834558-A2.
PD	08-APR-1998.
PF	02-OCT-1997; 117168.
PA	04-OCT-1996; JP-283314.
PA	(SUMO) SUMITOMO CHEM CO LTD.
PI	Koshiba T;
DR	WPI: 98-195460/18.
PT	P-PDSB; W57838.
PT	Aldehyde oxidase gene from plants and related vector and transformed
PT	cells - particularly for modulating auxin production in plants to
PT	accelerate maturation, increase yield, induce dwarfing etc.
PS	Claim 3: Page 30-34: 34pp; English.
CC	This sequence encodes the Zea mays aldehyde oxidase protein of the
CC	invention. The enzyme is able to oxidise an aldehyde to carboxylic ac
CC	(specifically indole acetaldehyde to indole acetic acid (auxin)). Cel
CC	transformed with the DNA are used to express the enzyme. Specificall
CC	expression of the DNA in transformed plants is used to increase (or
CC	suppress) production and activity of auxin, e.g. to cause earlier
CC	maturation of crops, improved yields and quality of fruit, to preven
CC	weak growth, to develop strains able to grow under suboptimal conditi
CC	to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
CC	flowers. Also plant cells that over-express the DNA can be proliferat
CC	differentiated and regenerated in sterile medium, particularly for
CC	production of virus-free nursery stock (of flowers or ornamental pla
QO	Sequence 4359 BP; 1146 A; 1056 C; 1138 G; 1019 T;

Query Match	62.9%	Score 17.6;	DB 1;	Length 4359;
Best Local Similarity	83.3%	Pred. No. 44;		
Matches 20;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0

Qy	1	GATTGCTGAACACACAAGATATGC	24
Db	2121	GATTGCTCAACACACAGAAGTATGC	2144

Search completed: July 15, 1999, 00:27:44

PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Claim 3; Page 30-34; 34pp; English.
 CC This sequence encodes the Zea mays aldehyde oxidase protein of the
 CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
 CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
 CC transformed with the DNA are used to express the enzyme. Specifically
 CC suppression of the DNA in transformed plants is used to increase (or
 CC suppress) production and activity of auxin, e.g. to cause earlier
 CC maturation of crops, improved yields and quality of fruit, to prevent
 CC weak growth, to develop strains able to grow under suboptimal conditions,
 CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
 CC flowers. Also plant cells that over express the DNA can be proliferated,
 CC differentiated and regenerated in sterile medium, particularly for
 CC production of virus-free nursery stock (of flowers or ornamental plants).
 SQ Sequence 4359 BP; 1146 A; 1056 C; 1138 G; 1019 T;

Query Match 100.0%; Score 25; DB 1; Length 4359;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCCATGTAGCATCTTC 25
 Db 2160 CTTGGCCCATGTAGCATCTTC 2136

RESULT 3
 T49387/c
 ID T49387 standard; DNA: 1075 BP.
 AC T49387;
 DT 23-AUG-1997 (first entry)
 DE Banana bunchy top virus DNA component 3.
 KW BBRV; intergenic region; promoter; transgenic plant; ds.
 OS Banana bunchy top virus.
 FH Key Location/Qualifiers
 FT stem_loop 1..31
 FT misc_binding /*tag= a
 FT 1..10
 FT /*tag= b
 FT /*note= "binds to nts 22-31"
 FT misc_structure 11..21
 FT /*tag= c
 FT /*note= "loop"
 FT 22..31
 FT /*tag= d
 FT /*note= "binds to nts 1-10"
 FT 1..44
 FT /*tag= e
 FT /*note= "stem loop common region"
 FT 189..197
 FT /*tag= f
 FT 213..740
 FT /*tag= g
 FT 704..709
 FT /*tag= h
 FT 755..760
 FT /*tag= i
 FT 786..875
 FT /*tag= j
 FT /*note= "major common region"
 FT 789..805
 FT /*tag= k
 FT /*rpt_type= DIRECT
 FT 806..821
 FT /*tag= l
 FT /*rpt_type= DIRECT
 FT 861..875
 FT /*tag= m
 FT /*note= "GC-rich sequence"
 WO9638554-A1.
 PD 05-DEC-1996. AU0335.
 PF 31-MAY-1996; AU0335.
 PR 31-MAY-1995; AU-003285.

PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
 PI Becker DK, Beetham PR, Dale JL, Dugdale B, Hafner GJ;
 PI Harding RM;
 DR WPI: 97-034368/03.
 DR P-PSDB; W09069.
 PT DNA from intergenic region of banana bunchy top virus DNA component
 PT - useful for promoting, enhancing, regulating or modifying
 PT transcription of a non-BBRV gene in transgenic plants
 PS Claim 4; Fig 1b; 80pp; English.
 CC Nucleotide sequences (T49386-90) are provided for banana bunchy top
 CC virus (BBRV) genomic components 2-6, which share stem-loop common
 CC regions (see also T49391-96) and major common regions. Component 3
 CC was isolated from a PCR library produced using primers (see also
 CC T49414-15) based on the conserved stem-loop and common major regions
 CC of components 1 and 2. It includes an open reading frame for a 175-
 CC amino acid polypeptide (W09069). The intergenic (non-coding)
 CC regions (see also T49399-409) of BBRV genomic components 1-6 have
 CC promoter activity (esp. components 2 and 6), and are useful for
 CC promoting, enhancing, regulating or modifying transcription of non-
 CC BBRV genes in monocotyledon or dicotyledon transgenic plants.
 SQ Sequence 1075 BP; 351 A; 199 C; 257 G; 268 T;

Query Match 68.0%; Score 17; DB 1; Length 1075;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTTGGCCCATGTAGCATCTTC 25
 Db 302 CTTGGCCCATGTAGCATCTTC 278

RESULT 4
 T49377/c
 ID T49377 standard; DNA: 1075 BP.
 AC T49377;
 DT 24-AUG-1997 (first entry)
 DE Banana bunchy top virus DNA component 3.
 KW BBRV; intergenic region; promoter; transgenic plant; ds.
 OS Banana bunchy top virus.
 FH Key Location/Qualifiers
 FT stem_loop 1..31
 FT misc_binding /*tag= a
 FT 1..10
 FT /*tag= b
 FT /*note= "binds to nts 22-31"
 FT misc_structure 11..21
 FT /*tag= c
 FT /*note= "loop"
 FT 22..31
 FT /*tag= d
 FT /*note= "binds to nts 1-10"
 FT 1..44
 FT /*tag= e
 FT /*note= "conserved stem loop common region"
 FT 189..197
 FT /*tag= f
 FT 213..740
 FT /*tag= g
 FT 704..709
 FT /*tag= h
 FT 755..760
 FT /*tag= i
 FT 786..875
 FT /*tag= j
 FT /*note= "conserved major common region"
 FT 789..805
 FT /*tag= k
 FT /*rpt_type= DIRECT
 FT 806..821
 FT /*tag= l
 FT /*rpt_type= DIRECT
 FT 861..875
 FT misc_feature

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OM nucleic - nucleic search, using sw model

Run on: July 15, 1999, 00:27:56 ; Search time 269.22 Seconds

(without alignments)
19.566 Million cell updates/sec

Title: US-08-943-144-13

Perfect score: 28
Sequence: 1 GATTGCTCAACACAGAGTATGCCTAC 28

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	4359	1 V40711	Aldehyde oxidase g
2	28	100.0	28	1 V40721	Primer for aldehyd
3	17.6	62.9	4412	1 V40710	Aldehyde oxidase g
4	17.6	62.9	28	1 V40715	Primer for aldehyd
5	17	60.7	5227	1 T79537	Plasmid pTERRA2H1
6	17	60.7	8353	1 T89396	Methods for diagno
7	16.8	60.0	80073	1 T58840-5	Continuation (6 of
8	16.8	60.0	9096	1 T88015	Human interleukin
9	16.8	60.0	1755	1 V03306	Bacterium OC9a pho
10	16.6	59.3	4698	1 Q32370	PIA genomic DNA. N
11	16.6	59.3	4698	1 Q72475	Entire PIA genomic
12	16.6	59.3	4698	1 T01176	P815A antigen prec
13	16.6	59.3	4698	1 T14692	MAGE genomic DNA.
14	16.4	58.6	3919	1 Q80418	Human mclur3 CDNA.
15	16.4	58.6	3410	1 T03887	Human mclur3 DNA.
16	16.4	58.6	2100	1 T70839	Mouse apoptosis in
17	16.4	58.6	251	1 V09952	Partial cDNA ineyt
18	16.4	58.6	2691	1 V55041	Murine XIAP coding
19	16.2	57.9	943	1 V22064	DNA encoding a krl
20	16.2	57.9	943	1 V22066	DNA encoding a krl
21	16	57.1	2153	1 Q06168	Encodes Human Bone
22	16	57.1	2153	1 Q29703	IRS-1. Purified nu
23	16	57.1	2153	1 Q32854	BMP5. Synergistic
24	16	57.1	336	1 Q41607	Transforming growt
25	16	57.1	2153	1 Q41295	Human BMP-5 gene.
26	16	57.1	411	1 Q60059	Human brain expres
27	16	57.1	336	1 T117239	Hybrid TGF-beta 3-
28	16	57.1	336	1 T15467	CDNA encoding huma
29	16	57.1	413	1 T92929	Streptococcus pneu
30	16	57.1	1215	1 T92928	Streptococcus pneu
31	16	57.1	3521	1 V52351	Sequence encoding
32	15.8	56.4	928	1 N92622	Sequence encoding
33	15.8	56.4	1475	1 N80638	Antigenic peptide
34	15.8	56.4	655	1 Q10911	Rat acyl peptide h
35	15.8	56.4	13206	1 Q05243	Factor VII CDNA of
36	15.8	56.4	2483	1 N60064	Glycoprotease gene
37	15.8	56.4	1315	1 Q27645	Encodes rabbit Hbl
38	15.8	56.4	2070	1 Q48515	Saporin/FGF fusion
39	15.8	56.4	1230	1 Q53899	K.lactis transalido
40	15.8	56.4	1349	1 Q57701	CDNA encoding Fact
41	15.8	56.4	1633	1 T00819	Mouse type-II memb
42	15.8	56.4	597	1 T00820	Mouse type-II memb
43	15.8	56.4	597	1 T00820	Mouse type-II memb

c 44 15.8 56.4 245 1 T20104 Human gene signatu
45 15.8 56.4 828 1 V61356 3' CDNA sequence o

ALIGNMENTS

```
RESULT 1
V40711
ID V40711 standard; CDNA to mRNA; 4359 BP.
AC V40711;
DT 22-SEP-1998 (first entry)
DE Aldehyde oxidase gene.
KW Aldehyde oxidase; auxin production; plant maturation; ss.
OS Zea mays.
FH Key
FT CDS Location/Qualifiers
FT CDS 91..4140
FT FT /*tag= a
PN EP-834558-A2.
PD 08-APR-1998.
PF 02-OCT-1997; 117168.
PR 04-OCT-1996; JP-283314.
PA (SUMO ) SUMITOMO CHEM CO LTD.
PI Koshiha T.
DR WPI: 98-195460/18.
DR P-PSDB: W57838.
PT Aldehyde oxidase gene from plants and related vector and transformed
PT cells - particularly for modulating auxin production in plants to
PT accelerate maturation, increase yield, induce dwarfing etc.
PS Claim 3: Page 30-34; 34pp; English.
CC This sequence encodes the Zea mays aldehyde oxidase protein of the
CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
CC transformed with the DNA are used to express the enzyme. Specifically
CC expression of the DNA in transformed plants is used to increase (or
CC suppress) production and activity of auxin, e.g. to cause earlier
CC maturation of crops, improved yields and quality of fruit, to prevent
CC weak growth, to develop strains able to grow under suboptimal conditions,
CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
CC flowers. Also plant cells that over-express the DNA can be proliferated,
CC differentiated and regenerated in sterile medium, particularly for
CC production of virus-free nursery stock (of flowers or ornamental plants).
SQ Sequence 4359 BP; 1146 A; 1056 C; 1138 G; 1019 T;
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Query Match 100.0%; Score 28; DB 1; Length 4359;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTGCTCAACACAGAGTATGCCTAC 28
DB 2121 GATTGCTCAACACAGAGTATGCCTAC 2148
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RESULT 2
V40721
ID V40721 standard; DNA; 28 BP.
AC V40721;
DT 22-SEP-1998 (first entry)
DE Primer for aldehyde oxidase gene.
KW Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.
OS Synthetic.
OS Zea mays.
PN EP-834558-A2.
PD 08-APR-1998.
PF 02-OCT-1997; 117168.
PR 04-OCT-1996; JP-283314.
PA (SUMO ) SUMITOMO CHEM CO LTD.
PI Koshiha T.
DR WPI: 98-195460/18.
PT Aldehyde oxidase gene from plants and related vector and transformed
PT cells - particularly for modulating auxin production in plants to
PT accelerate maturation, increase yield, induce dwarfing etc.
```

PS Example 8; Page 7; 34pp; English.
 CC This sequence represents a primer for the DNA encoding the Zea mays
 CC aldehyde oxidase protein of the invention. The enzyme is able to oxidise
 CC an aldehyde to carboxylic acid (specifically indole acetaldehyde to
 CC indole acetic acid (auxin)). Cells transformed with the DNA are used to
 CC express the enzyme. Specifically expression of the DNA in transformed
 CC plants is used to increase (or suppress) production and activity of
 CC auxin, e.g. to cause earlier maturation of crops, improved yields and
 CC quality of fruit, to prevent weak growth, to develop strains able to grow
 CC under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging
 CC in rice) and to shorten flowers. Also plant cells that over-express the
 CC DNA can be proliferated, differentiated and regenerated in sterile
 CC medium, particularly for production of virus-free nursery stock (of
 CC flowers or ornamental plants).
 SQ Sequence 28 BP; 10 A; 7 C; 5 G; 6 T;

Query Match 100.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GATTGCTCAACACAGAACTATGCTTAC 28
 DB 1 GATTGCTCAACACAGAACTATGCTTAC 28

RESULT 3
 V40710
 ID V40710: standard; cDNA to mRNA; 4412 BP.
 AC V40710:
 DT 22-SEP-1998 (first entry)
 DE Aldehyde oxidase gene.
 KW Aldehyde oxidase; auxin production; plant maturation; ss.
 OS Zea mays.
 FH Key Location/Qualifiers
 FT CDS 46..4122
 FT /*tag= a
 PN EP-834558-A2.
 PD 08-APR-1998.
 PF 02-OCT-1997; 117168.
 PR 04-OCT-1996; JP-283314.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Koshida T;
 DR WPI: 98-195460/18.
 DR P-PSDB; W57837.
 PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Claim 3; Page 17-21; 34pp; English.
 CC This sequence encodes the Zea mays aldehyde oxidase protein of the
 CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
 CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
 CC transformed with the DNA are used to express the enzyme. Specifically
 CC expression of the DNA in transformed plants is used to increase (or
 CC suppress) production and activity of auxin, e.g. to cause earlier
 CC maturation of crops, improved yields and quality of fruit, to prevent
 CC weak growth, to develop strains able to grow under suboptimal conditions,
 CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
 CC flowers. Also plant cells that over-express the DNA can be proliferated,
 CC differentiated and regenerated in sterile medium, particularly for
 CC production of virus-free nursery stock (of flowers or ornamental plants).
 SQ Sequence 4412 BP; 1193 A; 1061 C; 1142 G; 1016 T;

Query Match 62.9%; Score 17.6; DB 1; Length 4412;
 Best Local Similarity 83.3%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GATTGCTCAACACAGAACTATGCT 24
 DB 2100 GATTGCTCAACACAGAACTATGCT 2123

RESULT 4
 V40715
 ID V40715: standard; DNA; 28 BP.
 AC V40715:
 DT 22-SEP-1998 (first entry)
 DE Primer for aldehyde oxidase gene.
 KW Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.
 OS Synthetic.
 OS Zea mays.
 PN EP-834558-A2.
 PD 08-APR-1998.
 PF 02-OCT-1997; 117168.
 PR 04-OCT-1996; JP-283314.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Koshida T;
 DR WPI: 98-195460/18.
 PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Example 8; Page 7; 34pp; English.
 CC This sequence represents a primer for the DNA encoding the Zea mays
 CC aldehyde oxidase protein of the invention. The enzyme is able to oxidise
 CC an aldehyde to carboxylic acid (specifically indole acetaldehyde to
 CC indole acetic acid (auxin)). Cells transformed with the DNA are used to
 CC express the enzyme. Specifically expression of the DNA in transformed
 CC plants is used to increase (or suppress) production and activity of
 CC auxin, e.g. to cause earlier maturation of crops, improved yields and
 CC quality of fruit, to prevent weak growth, to develop strains able to grow
 CC under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging
 CC in rice) and to shorten flowers. Also plant cells that over-express the
 CC DNA can be proliferated, differentiated and regenerated in sterile
 CC medium, particularly for production of virus-free nursery stock (of
 CC flowers or ornamental plants).
 SQ Sequence 28 BP; 12 A; 4 C; 5 G; 7 T;

Query Match 62.9%; Score 17.6; DB 1; Length 28;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GATTGCTCAACACAGAACTATGCT 24
 DB 1 GATTGCTCAACACAGAACTATGCT 24

RESULT 5
 T79537/C
 ID T79537: standard; DNA; 5227 BP.
 AC T79537;
 DT 06-MAR-1998 (first entry)
 DE Plasmid pTERMSC2H10myc3SCAM.
 KW Protein-protein interaction; interacting polypeptide;
 KW polypease principle; plasmid pTERMSC2H10myc3SCAM; vector;
 KW Escherichia coli display; peptide library; ds.
 OS Synthetic.
 PN W09732017-A1.
 PD 04-SEP-1997.
 PF 26-FEB-1997; E00931.
 PR 26-FEB-1996; EP-102852.
 PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
 PI Ge L; Ilag V;
 DR WPI: 97-448687/41.
 PT Identification of interacting polypeptide encoding nucleic acid
 PT sequences - e.g. to identify protein-protein interactions, which
 PT play an important role in biological processes
 PS Example 8; Fig 25; 105pp; English.
 CC Plasmid pTERMSC2H10myc3SCAM (T79537) can be used in a novel method
 CC for identifying nucleic acid sequences (NAS), which encode
 CC polypeptides capable of interacting with at least 1 of their fellow
 CC polypeptides. This comprises: (a) providing a 1st library of
 CC recombinant vectors containing genetically diverse NAS comprising a
 CC variety of NAS encoding polypeptides; (b) providing a 2nd library of
 CC recombinant vectors containing genetically diverse NAS comprising a

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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 21:50:47 : Search time 189.37 Seconds
(without alignments)
11.619 Million cell updates/sec

ALIGNMENTS

c 38	14.2	59.2	1830	1	US-08-410-804-2	Sequence 2, Appl1
c 39	14.2	59.2	28958	1	US-08-258-251B-6	Sequence 6, Appl1
c 40	14.2	59.2	28958	2	US-08-456-837-6	Sequence 6, Appl1
c 41	14.2	59.2	28958	2	US-08-457-342-6	Sequence 6, Appl1
c 42	14.2	59.2	28958	2	US-08-457-646A-6	Sequence 6, Appl1
c 43	14.2	59.2	28958	2	US-08-458-076A-6	Sequence 6, Appl1
c 44	14.2	59.2	49377	2	US-08-764-233A-1	Sequence 1, Appl1
c 45	14.2	59.2	2403	4	US-08-463-483A-30	Sequence 30, Appl1

Title: US-08-943-144-12
Perfect score: 24
Sequence: 1 ATCGACTTGTGTGCGCCTTGAC 24

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database: Issued Patents, NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	16	66.7	791	4	US-08-467-603-67
c 3	16	66.7	793	4	US-08-467-603-69
c 4	16	66.7	774	4	US-08-467-603-71
c 5	16	66.7	998	4	US-08-467-603-73
c 6	15.8	65.8	163	4	US-08-272-514-1
c 7	15.6	65.0	490	1	US-08-133-711-43
c 8	15.6	65.0	2070	3	US-08-394-326-1
c 9	15.2	63.3	9785	1	US-08-319-387-1
c 10	15.2	63.3	1032	1	US-08-375-186-1
c 11	15.2	63.3	1032	2	US-08-457-797A-4
c 12	15.2	63.3	1032	2	US-08-813-025-4
c 13	15.2	63.3	1197	5	PCT-US94-14277-7
c 14	15	62.5	3278	1	US-07-778-880A-1
c 15	15	62.5	398	1	US-08-118-101A-5
c 16	15	62.5	49272	3	US-08-614-770A-1
c 17	15	62.5	1062	4	US-08-466-103A-13
c 18	15	62.5	4566	4	US-08-465-976A-1
c 19	14.8	61.7	1953	1	US-08-436-044-3
c 20	14.8	61.7	1953	4	US-08-436-044-3
c 21	14.8	61.7	1002	5	PCT-US95-08534-1
c 22	14.8	61.7	1953	5	PCT-US95-08512-3
c 23	14.6	60.8	5496	1	US-08-181-629A-2
c 24	14.6	60.8	7001	1	US-08-258-251B-1
c 25	14.6	60.8	7001	2	US-08-456-837-1
c 26	14.6	60.8	7001	2	US-08-457-342-1
c 27	14.6	60.8	7001	2	US-08-457-646A-1
c 28	14.6	60.8	7001	2	US-08-458-076A-1
c 29	14.6	60.8	7001	2	US-08-457-335A-1
c 30	14.6	60.8	7001	3	US-08-761-258-6
c 31	14.6	60.8	7001	3	US-08-729-214-1
c 32	14.4	60.0	2563	1	US-08-423-441-1
c 33	14.4	60.0	38	2	US-08-373-124A-1095
c 34	14.4	60.0	5300	3	US-08-766-014-1
c 35	14.4	60.0	38	3	US-08-435-628-1095
c 36	14.2	59.2	1611	1	US-08-061-062A-5
c 37	14.2	59.2	3250	1	US-08-061-062A-7

RESULT 1
US-08-729-214-23/c
Sequence 23, Application US/08729214
Patent No. 5817502
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: van Pee, Karl-Helinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
antipathogenic substances
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 615..2228
OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 of DNA sequence"
FEATURE:
NAME/KEY: CDS
LOCATION: 2231..3313
OTHER INFORMATION: /label= ORF2
OTHER INFORMATION: /note= "Open Reading Frame #2 of DNA sequence"
FEATURE:
NAME/KEY: CDS
LOCATION: 3368..5065
OTHER INFORMATION: /label= ORF3
OTHER INFORMATION: /note= "Open Reading Frame #3 of DNA sequence"

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 21:50:26 ; Search time 189.37 Seconds
(without alignments)
11.135 Million cell updates/sec

Title: US-08-943-144-6

Perfect score: 23 GCGGAGCGCTGTATGTCAGCA 23

Scoring table: IDENTITY_NMC

Searched: 176461 seqs, 45838279 residues

Database: Issued_Patents_NA.*

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5: /cgn2_6/ptodata1/1na/PCTUS9_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.2	66.1	3319	1	US-08-006-676B-2	Sequence 2, Appl1
2	15.2	66.1	3319	2	US-08-282-845-1	Sequence 1, Appl1
3	15.2	66.1	3319	5	PCT-US94-00324-2	Sequence 2, Appl1
4	14.6	63.5	5738	2	US-08-409-995-3	Sequence 3, Appl1
5	14.6	63.5	1650	3	US-08-399-561-5	Sequence 5, Appl1
6	14.6	63.5	28804	4	US-08-592-874-1	Sequence 1, Appl1
7	14.2	61.7	2291	1	US-07-872-644-5	Sequence 5, Appl1
8	14.2	61.7	2656	1	US-07-872-644-16	Sequence 16, Appl1
9	14.2	61.7	1844	1	US-07-872-644-26	Sequence 48, Appl1
10	14.2	61.7	1625	1	US-07-872-644-48	Sequence 5, Appl1
11	14.2	61.7	2291	1	US-08-297-494-5	Sequence 16, Appl1
12	14.2	61.7	2656	1	US-08-287-494-16	Sequence 26, Appl1
13	14.2	61.7	1844	1	US-08-297-494-26	Sequence 48, Appl1
14	14.2	61.7	1625	1	US-08-297-510-5	Sequence 5, Appl1
15	14.2	61.7	2291	1	US-08-297-510-16	Sequence 16, Appl1
16	14.2	61.7	2656	1	US-08-297-510-26	Sequence 26, Appl1
17	14.2	61.7	1844	1	US-08-297-510-48	Sequence 48, Appl1
18	14.2	61.7	1625	1	US-08-313-681A-1	Sequence 3, Appl1
19	14.2	61.7	2291	1	US-08-313-681A-16	Sequence 16, Appl1
20	14.2	61.7	2656	1	US-08-118-101A-3	Sequence 14, Appl1
21	14.2	61.7	1116	3	US-08-244-646-14	Sequence 16, Appl1
22	14.2	61.7	792	3	US-08-244-646-16	Sequence 16, Appl1
23	14.2	61.7	2219	3	US-08-606-322-1	Sequence 5, Appl1
24	14.2	61.7	2291	3	US-08-479-532-5	Sequence 16, Appl1
25	14.2	61.7	2656	3	US-08-479-532-16	Sequence 26, Appl1
26	14.2	61.7	1844	3	US-08-479-532-26	Sequence 48, Appl1
27	14.2	61.7	1625	3	US-08-479-532-48	Sequence 48, Appl1
28	14.2	61.7	2917	3	US-08-592-936B-20	Sequence 20, Appl1
29	14.2	61.7	2291	3	US-08-455-526-5	Sequence 5, Appl1
30	14.2	61.7	2656	3	US-08-455-526-16	Sequence 16, Appl1
31	14.2	61.7	1844	3	US-08-455-526-26	Sequence 26, Appl1
32	14.2	61.7	1625	3	US-08-455-526-48	Sequence 48, Appl1
33	14.2	61.7	2291	3	US-08-455-525-5	Sequence 5, Appl1
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36	14.2	61.7	1625	3	US-08-455-525-48	Sequence 48, Appl1
37	14.2	61.7	2265	4	US-08-940-332-1	Sequence 1, Appl1

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39	14.2	61.7	2291	5	PCT-US92-03222-5	Sequence 5, Appl1
40	14.2	61.7	2656	5	PCT-US92-03222-16	Sequence 16, Appl1
41	14.2	61.7	1844	5	PCT-US92-03222-26	Sequence 26, Appl1
42	14.2	61.7	1625	5	PCT-US92-03222-48	Sequence 48, Appl1
43	14.2	60.9	436	1	US-07-956-700B-110	Sequence 110, Appl1
44	14.2	60.9	436	3	US-08-476-537-110	Sequence 110, Appl1
45	14.2	60.9	3432	5	PCT-US95-04589-141	Sequence 141, Appl1

ALIGNMENTS

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RESULT 1
US-08-006-676B-2
; Sequence 2, Application US/08006676B
; Patent No. 541865
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey B. Oster
; STREET: 8339 SE 57th Street
; CITY: Mercer Island
; STATE: Washington
; COUNTRY: USA
; ZIP: 98040-4906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/006, 676B
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: REED-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 232 7845
; TELEFAX: (206) 236 0205
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3319 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Leishmania chagasi
; US-08-006-676B-2

Query Match
Best local similarity 66.1%; Score 15.2; DB 1; Length 3319;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGGAGCGCTGTATGTCAGC 22
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RESULT 2
US-08-282-845-1
; Sequence 1, Application US/08282845
; Patent No. 5719263
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: A 230kD Antigen Present in Leishmania
; TITLE OF INVENTION: Species
```

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System 7.1
SOFTWARE: Microsoft Word for Macintosh 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FK39
FEATURE:
NAME/KEY: CDS
LOCATION: 455..3319
US-08-282-845-1

Query Match 66.1%; Score 15.2; DB 2; Length 3319;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGNGARGCNGTATGTCNGAYG 22
DB 1049 GGCGAGGAGGTGACGTGCAGC 1070

RESULT 3
PCT-US94-00324-2
Sequence 2, Application PC/TUS9400324
GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version 5.1a

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Leishmania chagasi
PCT-US94-00324-2

Query Match 66.1%; Score 15.2; DB 5; Length 3319;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGNGARGCNGTATGTCNGAYG 22
DB 1049 GGCGAGGAGGTGACGTGCAGC 1070

RESULT 4
US-08-409-995-3/c
Sequence 3, Application US/08409995
Patent No. 5646259
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen I.
TITLE OF INVENTION: St. Game IIT, Joseph W.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobach, Test, Albrighton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5738 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 1999, 00:27:34 ; Search time 269.22 Seconds

(without alignments)
16.072 Million cell updates/sec

Title: US-08-943-144-6

Perfect score: 23

Sequence: 1 GCGGARGCGTGTATGATGAYGA 23

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17.8	77.4	4412	1	V40710	Aldehyde oxidase g
2	17.8	77.4	4359	1	V40711	Aldehyde oxidase g
3	17.8	77.4	23	1	V40713	Primer for aldehyd
4	15.2	66.1	3319	1	O70152	K39 gene of Leishm
5	15.2	66.1	3319	1	T42166	Leishmania chagasi
6	15.2	66.1	110000	1	V21209_08	Continuation (9 of
7	14.8	64.3	2777	1	T41849	Bacillus cellulase
8	14.6	63.5	3683	1	O85999	Thermotoga pullu
9	14.6	63.5	1782	1	T04121	P. gingivalis cell
10	14.6	63.5	6000	1	T06308	Arabidopsis pathog
11	14.6	63.5	1782	1	T18119	Porphyromonas ging
12	14.6	63.5	28804	1	T37329	Sphingaria biosynt
13	14.6	63.5	1650	1	T40207	Tomato lycopen
14	14.6	63.5	7291	1	T41476	Haemophilus adhe
15	14.6	63.5	7000	1	T37476	RPP5 downy mildew
16	14.6	63.5	1942	1	T42979	Capiscum annuum
17	14.6	63.5	28804	1	T92474	Sphingomonas genu
18	14.2	61.7	2281	1	O30163	PCAM-40 clone cont
19	14.2	61.7	2656	1	O30172	Bovine lung 59 kD
20	14.2	61.7	1844	1	O30175	63 kD CAM PDE cDN
21	14.2	61.7	1117	1	O42595	Sequence encoding
22	14.2	61.7	792	1	O42596	Sequence of varian
23	14.2	61.7	584	1	O55684	Human CAP18 gene
24	14.2	61.7	1625	1	O83980	Cyclic-GMP stimula
25	14.2	61.7	1844	1	O83989	Cyclic-GMP stimula
26	14.2	61.7	2656	1	O83964	Cyclic-GMP stimula
27	14.2	61.7	2291	1	O83957	Cyclic-GMP stimula
28	14.2	61.7	2659	1	O82793	TRK2 gene. New tra
29	14.2	61.7	615	1	T18233	Prepro-PAL-99 cDN
30	14.2	61.7	2219	1	T36646	Acetabiose biosynt
31	14.2	61.7	2656	1	T51091	Coding sequence fo
32	14.2	61.7	2291	1	T51094	61 kD brain calciu
33	14.2	61.7	1844	1	T51105	cDNA for 63 kD cal
34	14.2	61.7	1625	1	T51115	Hippocampus calciu
35	14.2	61.7	2291	1	T67198	Bovine brain Ca2+/
36	14.2	61.7	2656	1	T67199	Bovine lung 59 kDa
37	14.2	61.7	1844	1	T67200	Bovine brain 63 kDa
38	14.2	61.7	1625	1	T67201	Human brain 61 kDa
39	14.2	61.7	6749	1	T47564	Cytomegalovirus pp
40	14.2	61.7	3141	1	T47556	Human cytomegalovir
41	14.2	61.7	4075	1	T47557	42k promoted cytom
42	14.2	61.7	4909	1	T47558	42k promoted cytom
43	14.2	61.7	3367	1	T47559	42k promoted cytom

ALIGNMENTS

44 14.2 61.7 6749 1 T47561
45 14.2 61.7 17935 1 V56642

Cytomegalovirus pp
Actinoplanes sp. a

RESULT. 1

V40710
ID V40710 standard; cDNA to mRNA; 4412 BP.

AC V40710:
DT 22-SEP-1998 (first entry)

DE Aldehyde oxidase gene.

KW Aldehyde oxidase; auxin production; plant maturation; ss.

OS Zea mays.

FH Key Location/Qualifiers

FT CDS 46..412

FT CDS /*tag= a

FN EP-834558-A2.

PD 08-APR-1998.

PF 02-OCT-1997; 117168.

PA 04-OCT-1996; JP-283314.

PR (SUMO) SUMITOMO CHEM CO LTD.

PI Koshiha T.

DR WPT: 98-195460/18.

P-PSDB: W57837.

PT Aldehyde oxidase gene from plants and related vector and transformed

PS cells - particularly for modulating auxin production in plants to

accelerate maturation, increase yield, induce dwarfing etc.

CC Claim 3, Page 17-21; 34pp. English.

CC This sequence encodes the Zea mays aldehyde oxidase protein of the

CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid

CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells

CC transformed with the DNA are used to express the enzyme. Specifically

CC expression of the DNA in transformed plants is used to increase (or

CC suppress) production and activity of auxin, e.g. to cause earlier

CC maturation of crops, improved yields and quality of fruit, to prevent

CC weak growth, to develop strains able to grow under suboptimal conditions,

CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten

CC flowers. Also plant cells that over-express the DNA can be proliferated,

CC differentiated and regenerated in sterile medium, particularly for

CC production of virus-free nursery stock (of flowers or ornamental plants).

CC Sequence 4412 BP; 1193 A; 1061 C; 1142 G; 1016 T;

Query Match 77.4%; Score 17.8; DB 1; Length 4412;

Best Local Similarity 69.6%; Pred. No. 1.8;

Matches 16; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCGGARGCGTGTATGATGAYGA 23

DB 1840 GCGGARGCGTGTATGATGAYGA 1862

RESULT 2

ID V40711 standard; cDNA to mRNA; 4359 BP.

AC V40711:

DT 22-SEP-1998 (first entry)

DE Aldehyde oxidase gene.

KW Aldehyde oxidase; auxin production; plant maturation; ss.

OS Zea mays.

FH Key Location/Qualifiers

FT CDS 91..4140

FT CDS /*tag= a

FN EP-834558-A2.

PD 08-APR-1998.

PF 02-OCT-1997; 117168.

PA 04-OCT-1996; JP-283314.

PR (SUMO) SUMITOMO CHEM CO LTD.

PI Koshiha T.

DR WPT: 98-195460/18.

P-PSDB: W57838.

PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Claim 3; Page 30-34; 34pp: English.
 CC This sequence encodes the zea mays aldehyde oxidase protein of the
 CC invention. The enzyme is able to oxidise an aldehyde to carboxylic acid
 CC (specifically indole acetaldehyde to indole acetic acid (auxin)). Cells
 CC transformed with the DNA are used to express the enzyme. Specifically
 CC suppression of production and activity of auxin, e.g. to cause earlier
 CC maturation of crops, improved yields and quality of fruit, to prevent
 CC weak growth, to develop strains able to grow under suboptimal conditions,
 CC to induce dwarfing (e.g. to inhibit lodging in rice) and to shorten
 CC flowers. Also plant cells that over-express the DNA can be proliferated,
 CC differentiated and regenerated in sterile medium, particularly for
 CC production of virus-free nursery stock (of flowers or ornamental plants).
 SO Sequence 4359 BP; 1146 A; 1056 C; 1138 G; 1019 T;

Query Match 77.4%; Score 17.8; DB 1; Length 4359;
 Best Local Similarity 69.6%; Pred. No. 1.8;
 Matches 16; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 GGNGARGCNGTNTAYGTNGAYCA 23
 Db 1858 GGGGAGAGCTGTCTACCTTGATCA 1880

RESULT 3
 ID V40713 standard; DNA: 23 BP.
 AC V40713;
 DT 22-SEP-1998 (first entry)
 DE Primer for aldehyde oxidase gene.
 KW Aldehyde oxidase; auxin production; plant maturation; PCR primer; ss.
 OS Synthetic.
 FH Zea mays.
 FT key Location/Qualifiers
 FT modified_base 3
 FT /*tag= a
 FT /mod_base= 1
 FT modified_base 9
 FT /*tag= b
 FT /mod_base= 1
 FT modified_base 12
 FT /*tag= c
 FT /mod_base= 1
 FT modified_base 18
 FT /*tag= d
 FT /mod_base= 1

EP-834558-A2.
 PN 08-APR-1998.
 PF 02-OCT-1997; 117168.
 PR 04-OCT-1996; JP-283314.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Koshida T.
 DR WPI: 98-15460/18.
 PT Aldehyde oxidase gene from plants and related vector and transformed
 PT cells - particularly for modulating auxin production in plants to
 PT accelerate maturation, increase yield, induce dwarfing etc.
 PS Example 6; Page 7; 34pp: English.
 CC This sequence represents a primer for the DNA encoding the zea mays
 CC aldehyde oxidase protein of the invention. The enzyme is able to oxidise
 CC an aldehyde to carboxylic acid (specifically indole acetaldehyde to
 CC indole acetic acid (auxin)). Cells transformed with the DNA are used to
 CC express the enzyme. Specifically expression of the DNA in transformed
 CC plants is used to increase (or suppress) production and activity of
 CC auxin, e.g. to cause earlier maturation of crops, improved yields and
 CC quality of fruit, to prevent weak growth, to develop strains able to grow
 CC under suboptimal conditions, to induce dwarfing (e.g. to inhibit lodging
 CC in rice) and to shorten flowers. Also plant cells that over-express the
 CC DNA can be proliferated, differentiated and regenerated in sterile
 CC medium, particularly for production of virus-free nursery stock (of

CC flowers or ornamental plants).
 SO Sequence 23 BP; 4 A; 1 C; 8 G; 3 T;

Query Match 77.4%; Score 17.8; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGNGARGCNGTNTAYGTNGAYCA 23
 Db 1 GGNGARGCNGTNTAYGTNGAYCA 23

RESULT 4
 ID 070152 standard; cDNA to mRNA; 3319 BP.
 AC 070152;
 DT 08-MAR-1995 (first entry)
 DE K39 gene of Leishmania chagasi.
 KW Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
 KW Leishmania chagasi; ss.
 OS Leishmania chagasi.
 FH key Location/Qualifiers
 FT cds 455..3319
 FT /*tag= a
 FT /product= K39.
 FT MO9416331-A.
 PN 21-JUL-1994.
 PF 10-JAN-1994; U00324.
 PR 15-JAN-1993; US-006676.
 PA (IASY-) IASYS CORP.
 PI Reed SG;
 DR WPI: 94-249402/30.
 DR P-PSTDB: R57365.
 PT Diagnosis of Leishmaniasis - by determining the presence of
 PT antibodies that bind to a K39 repeat unit antigen
 PS Disclosure; Page 15-17; 28pp: English.
 CC The K39 gene encodes a polypeptide which comprises a number of
 CC repeated units (described in R57365). Detection of antibodies
 CC directed against this repeated unit in a patients sample is
 CC indicative of Leishmaniasis. The antigenic repeat unit can
 CC itself be used as a vaccine to protect against infection by a
 CC Leishmania parasite.
 SO Sequence 3319 BP; 669 A; 969 C; 1196 G; 485 T;

Query Match 66.1%; Score 15.2; DB 1; Length 3319;
 Best Local Similarity 63.6%; Pred. No. 38;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 GGNGARGCNGTNTAYGTNGAYC 22
 Db 1049 GCGGAGAGAGTGTACTGAGACG 1070

RESULT 5
 ID T42166 standard; DNA: 3319 BP.
 AC T42166;
 DT 09-MAR-1997 (first entry)
 DE Leishmania chagasi K39 antigen.
 KW Leishmania chagasi; acidic ribosomal antigen; LcP0;
 KW epitope; K39; ss.
 OS Leishmania chagasi.
 FH key Location/Qualifiers
 FT cds 455..3319
 FT /*tag= a
 FT MO9633414-A2.
 PN 24-OCT-1996.
 PF 19-APR-1996; U05472.
 PR 21-APR-1995; US-428414.
 PA (COR-) CORIXA CORP.
 PI Reed SG;

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 23:44:04 ; Search time 4576.22 Seconds
(without alignments)
17.981 Million cell updates/sec

Title: US-08-943-144-5
Perfect score: 1 GTCCANGTNCCTCTGMAINAC 23
Sequence: 1

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database:

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2: gb_ba2.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl1.*
9: gb_pl2.*
10: gb_pl3.*
11: gb_pl4.*
12: gb_pl5.*
13: gb_pl6.*
14: gb_pl7.*
15: gb_pl8.*
16: gb_pl9.*
17: gb_pl10.*
18: gb_pl11.*
19: gb_pl12.*
20: gb_pl13.*
21: gb_pl14.*
22: gb_pl15.*
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27: gb_pl20.*
28: gb_pl21.*
29: gb_pl22.*
30: gb_pl23.*
31: gb_pl24.*
32: gb_pl25.*
33: gb_pl26.*
34: gb_pl27.*
35: gb_pl28.*
36: gb_pl29.*
37: gb_pl30.*
38: gb_pl31.*
39: gb_pl32.*
40: gb_pl33.*
41: gb_pl34.*
42: gb_pl35.*
43: gb_pl36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

Result	Query	Match	Length	DB	ID	Description
1	73.9	4382	8	D88451		D88451 Zea mays mr
2	17	73.9	8	D88452		D88452 Zea mays mr
3	17	73.9	8	SPU33214		U33214 Schizosacch
4	17	73.9	8	D88451		D88451 Zea mays mr
5	17	73.9	8	D88452		D88452 Zea mays mr
6	17	73.9	8	SPU33214		U33214 Schizosacch
7	16	69.6	11	YXYXLRN		L18965 Thermophil
8	16	69.6	11	HSAC002074		AC002074 Human BAC
9	16	69.6	11	YXYXLRN		L18965 Thermophil
10	16	69.6	11	HSAC002074		AC002074 Human BAC
11	15.4	67.0	3	CEFS4B3		Z48583 Caenorhabdi
12	15.4	67.0	3	L49408		L49408 Drosophila
13	15.4	67.0	3	SSRP3		X9334 S.scrofa mr
14	15.4	67.0	3	ANGNPRB		D25417 Bel mRNA fo
15	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
16	15.4	67.0	3	AC005760		AC005760 Homo sapi
17	15.4	67.0	3	AC006115		AC006115 Homo sapi
18	15.4	67.0	3	MOSGLUT1		D10229 Mus musculu
19	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
20	15.4	67.0	3	AC005760		AC005760 Homo sapi
21	15.4	67.0	3	AC006115		AC006115 Homo sapi
22	15.4	67.0	3	CEFS4B3		Z48583 Caenorhabdi
23	15.4	67.0	3	L49408		L49408 Drosophila
24	15.4	67.0	3	SSRP3		X9334 S.scrofa mr
25	15.4	67.0	3	ANGNPRB		D25417 Bel mRNA fo
26	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
27	15.4	67.0	3	AC005760		AC005760 Homo sapi
28	15.4	67.0	3	AC006115		AC006115 Homo sapi
29	15.4	67.0	3	MOSGLUT1		D10229 Mus musculu
30	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
31	15.4	67.0	3	AC005760		AC005760 Homo sapi
32	15.4	67.0	3	AC006115		AC006115 Homo sapi
33	15.4	67.0	3	CEFS4B3		Z48583 Caenorhabdi
34	15.4	67.0	3	L49408		L49408 Drosophila
35	15.4	67.0	3	SSRP3		X9334 S.scrofa mr
36	15.4	67.0	3	ANGNPRB		D25417 Bel mRNA fo
37	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
38	15.4	67.0	3	AC005760		AC005760 Homo sapi
39	15.4	67.0	3	AC006115		AC006115 Homo sapi
40	15.4	67.0	3	MOSGLUT1		D10229 Mus musculu
41	15.4	67.0	3	YUP8H12R		AC002986 Arabidops
42	15.4	67.0	3	AC005760		AC005760 Homo sapi
43	15.4	67.0	3	AC006115		AC006115 Homo sapi
44	15.4	67.0	3	CEFS4B3		Z48583 Caenorhabdi
45	15.4	67.0	3	L49408		L49408 Drosophila

ALIGNMENTS

RESULT 1
D88451/c 4382 bp mRNA PLN 10-NOV-1997
LOCUS D88451
DEFINITION Zea mays mRNA for aldehyde oxidase, complete cds.
ACCESSION D88451
NID 92589161
KEYWORDS aldehyde oxidase; zmao-1.
SOURCE Zea mays coleoptile cDNA to mRNA.
ORGANISM Zea mays

REFERENCE
AUTHORS Sekimoto, H., Seo, M., Dohme, N., Takio, K., Kamiya, Y. and Koshida, T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase
JOURNAL U. Biol. Chem. 272 (24), 15280-15285 (1997)
MEDLINE 97326103
REFERENCE 2 (bases 1 to 4382)
AUTHORS Sekimoto, H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hirotsuki Sekimoto, The Institute of Physical and Chemical Research,
Frontier Research Program, Hirotsuki 2-1, Wako, Saitama 351-01,

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 14, 1999, 21:50:51 ; Search time 189.37 seconds
(without alignments)
11.619 Million cell updates/sec

Title: US-08-943-144-15

Perfect score: 24
Sequence: 1 TTCACCTAGGTGTCAGTGTTC 24

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database:

Issued_Patents_NA:*
1: /cgn2-6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2-6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2-6/ptodata/1/ina/5C.COMB.seq:*
4: /cgn2-6/ptodata/1/ina/5D.COMB.seq:*
5: /cgn2-6/ptodata/1/ina/PT059.COMB.seq:*
6: /cgn2-6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19.2	80.0	2093	2	US-08-295-814E-5	Sequence 5, Appl
C 2	19.2	80.0	2093	5	PCT-US93-01959-5	Sequence 5, Appl
C 3	16	66.7	218	1	US-08-248-474-100	Sequence 100, App
4	15.2	63.3	10596	1	US-07-884-811-15	Sequence 15, Appl
5	15.2	63.3	10596	1	US-07-885-971-15	Sequence 15, Appl
6	15.2	63.3	10596	1	US-08-087-783A-15	Sequence 15, Appl
7	15.2	63.3	6911	1	US-08-311-174-4	Sequence 4, Appl
8	15.2	63.3	10596	1	US-08-194-088B-15	Sequence 15, Appl
9	15.2	63.3	10596	4	US-08-194-087-15	Sequence 15, Appl
10	15.2	63.3	8575	5	PCT-US92-08258-6	Sequence 15, Appl
11	15.2	63.3	10596	5	PCT-US93-04648-15	Sequence 15, Appl
12	15	62.5	2174	1	US-07-817-917-2	Sequence 2, Appl
13	15	62.5	2834	2	US-08-477-251A-1	Sequence 1, Appl
14	15	62.5	5319	3	US-08-169-927-1	Sequence 1, Appl
15	14.8	61.7	5577	2	US-08-326-117B-1	Sequence 1, Appl
16	14.8	61.7	630	3	US-08-580-038-73	Sequence 73, Appl
17	14.8	61.7	632	3	US-08-580-038-77	Sequence 77, Appl
18	14.8	61.7	3450	4	US-08-545-562A-6	Sequence 6, Appl
19	14.8	61.7	3471	5	PCT-US93-00227-2	Sequence 2, Appl
20	14.6	60.8	100	6	5179196-1	Patent No. 5179196
21	14.4	60.0	1470	1	US-08-124-674-1	Sequence 1, Appl
22	14.4	60.0	1320	1	US-08-176-412-1	Sequence 1, Appl
23	14.4	60.0	4154	1	US-08-131-365B-37	Sequence 37, Appl
24	14.4	60.0	1470	3	US-08-589-893-1	Sequence 1, Appl
25	14.4	60.0	1470	3	US-08-589-893-3	Sequence 3, Appl
26	14.4	60.0	1470	3	US-08-589-893-5	Sequence 5, Appl
27	14.4	60.0	1470	3	US-08-589-893-7	Sequence 7, Appl
28	14.4	60.0	1470	3	US-08-589-893-9	Sequence 9, Appl
29	14.4	60.0	1470	3	US-08-589-893-11	Sequence 11, Appl
30	14.4	60.0	1470	3	US-08-589-893-13	Sequence 13, Appl
31	14.4	60.0	1470	3	US-08-589-893-15	Sequence 15, Appl
32	14.4	60.0	1470	3	US-08-589-893-17	Sequence 17, Appl
33	14.4	60.0	1470	3	US-08-589-893-19	Sequence 19, Appl
34	14.4	60.0	1470	3	US-08-589-893-21	Sequence 21, Appl
35	14.4	60.0	1470	3	US-08-589-893-23	Sequence 23, Appl
36	14.4	60.0	7070	3	US-08-619-554-3	Sequence 3, Appl
C 37	14.4	60.0	4877	4	US-08-404-531B-7	Sequence 7, Appl

ALIGNMENTS

C 38	14.4	60.0	4877	4	US-08-404-531B-8	Sequence 8, Appl
C 39	14.4	60.0	2112	4	US-08-861-464-9	Sequence 9, Appl
C 40	14.4	60.0	1608	5	PCT-US94-02891-68	Sequence 68, Appl
C 41	14.4	60.0	1320	5	PCT-US94-14436-1	Sequence 1, Appl
C 42	14.2	59.2	843	3	US-08-040-548-9	Sequence 9, Appl
C 43	14.2	59.2	3086	3	US-08-040-548-15	Sequence 15, Appl
C 44	14.2	59.2	843	3	US-08-466-344-9	Sequence 9, Appl
C 45	14.2	59.2	3086	3	US-08-466-344-15	Sequence 15, Appl

RESULT 1
US-08-295-814E-5/C
Sequence 5, Application US/08295814E
Patent No. 5658786
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Hartig, Paul R.
APPLICANT: Weinschenk, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
TITLE OF INVENTION: TRANSPORTERS AND USBS THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,814E
FILING DATE: DECEMBER 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40558-B-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2093 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Taurine
IMMEDIATE SOURCE:
LIBRARY: rat brain
CLONE: r16a
FEATURE:
NAME/KEY: CDS
LOCATION: 127..1989
OTHER INFORMATION:
US-08-295-814E-5

Query Match 80.0%; Score 19.2; DB 2; Length 2093;
Best Local Similarity 87.5%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTCACCTATGTTGCACTGTTCC 24
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Db 626 TTCACCTATGTTGCACTGTTCC 603

RESULT 2
PCT-US93-01959-5/c
; Sequence 5, Application PC/TUS9301959
; GENERAL INFORMATION:
; APPLICANT: Smith, E. Kelli
; APPLICANT: Borden, A. Laurence
; APPLICANT: Hartig, R. Paul
; APPLICANT: Weinschenk, L. Richard
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01959
; FILING DATE: 19930304
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40558A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEFAX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2093 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Taurine
; IMMEDIATE SOURCE:
; LIBRARY: rat brain
; CLONE: rb16a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..1989
; OTHER INFORMATION:
PCT-US93-01959-5

Query Match 80.0%; Score 19.2; DB 5; Length 2093;
Best Local Similarity 87.5%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 3

OY 1 TTCACCTATGTTGCACTGTTCC 24
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Db 626 TTCACCTATGTTGCACTGTTCC 603

US-08-248-474-100/c
; Sequence 100, Application US/08248474
; Patent No. 5612471
; GENERAL INFORMATION:
; APPLICANT: MCK. BIRD, David
; APPLICANT: WILSON, Mark A.
; TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,474
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 2307E-535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum cv 'Rutgers Large
; ORGANISM: Red'
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..218
; OTHER INFORMATION: /standard_name="DB# 265"

US-08-248-474-100
Query Match 66.7%; Score 16; DB 1; Length 218;
Best Local Similarity 79.2%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTCACCTATGTTGCACTGTTCC 24
|||||
Db 71 TTCACCTATGTTGCACTGTTCC 48

RESULT 4
US-07-884-811-15
; Sequence 15, Application US/07884811
; Patent No. 5316921
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM: